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## OM protein - protein search, using sw model

Run on: September 19, 2002, 17:29:22 : Search time 23.54 Seconds  
(without alignments)  
321.662 Million cell updates/sec

Title: US-09-524-531C-13  
Perfect score: 1633  
Sequence: 1 MALSRRLRLVRLAPLPHFL.....VNVTSESGDFRHKSSFVY 310

## Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 2442594 residues

● 1 number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PTOUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                | Description        |
|------------|-------|-------------|--------|-------------------|--------------------|
| 1          | 415   | 25.4        | 299    | US-09-188-930-331 | Sequence 331, App  |
| 2          | 415   | 25.4        | 299    | US-09-462-270-2   | Sequence 2, Appli  |
| 3          | 403   | 24.7        | 299    | US-09-188-930-189 | Sequence 189, App  |
| 4          | 283   | 17.3        | 205    | US-09-462-270-4   | Sequence 4, Appli  |
| 5          | 242.5 | 14.8        | 319    | US-08-597-495B-22 | Sequence 22, Appl  |
| 6          | 240.5 | 14.7        | 318    | US-09-068-051A-22 | Sequence 22, Appl  |
| 7          | 240.5 | 14.7        | 318    | US-09-068-051A-32 | Sequence 32, Appli |
| 8          | 197.5 | 12.1        | 387    | US-09-175-928-2   | Sequence 2, Appli  |
| 9          | 173.5 | 10.6        | 365    | US-08-928-383B-2  | Sequence 3, Appli  |
| 10         | 172.5 | 10.6        | 365    | US-08-979-424-3   | Sequence 2, Appli  |
| 11         | 172.5 | 10.6        | 365    | US-09-272-496-2   | Sequence 2, Appli  |
| 12         | 171.5 | 10.5        | 390    | US-08-979-424-1   | Sequence 1, Appli  |
| 13         | 166   | 10.2        | 1101   | US-08-986-485-2   | Sequence 2, Appli  |
| 14         | 160   | 9.8         | 869    | US-08-374-834-16  | Sequence 16, Appl  |
| 15         | 160   | 9.8         | 869    | US-08-644-271-29  | Sequence 29, Appl  |
| 16         | 156.5 | 9.6         | 365    | US-08-928-383B-23 | Sequence 24, Appl  |
| 17         | 156.5 | 9.6         | 365    | US-08-928-383B-24 | Sequence 24, Appl  |
| 18         | 151.5 | 9.3         | 365    | US-08-928-383B-26 | Sequence 26, Appl  |
| 19         | 151   | 9.2         | 1091   | US-08-986-485-5   | Sequence 5, Appli  |
| 20         | 150   | 9.2         | 1297   | US-08-540-245A-17 | Sequence 17, Appl  |
| 21         | 148   | 9.1         | 607    | US-08-752-307B-12 | Sequence 12, Appl  |
| 22         | 147.5 | 9.0         | 501    | US-08-408-095-31  | Sequence 31, Appl  |
| 23         | 147   | 9.0         | 95     | US-08-928-383B-18 | Sequence 18, Appl  |
| 24         | 147   | 9.0         | 1395   | US-09-540-245A-15 | Sequence 15, Appl  |
| 25         | 146.5 | 9.0         | 478    | PCT-US95-08493-15 | Sequence 15, Appl  |
| 26         | 146.5 | 9.0         | 860    | PCT-US95-08493-19 | Sequence 19, Appl  |
| 27         | 146.5 | 9.0         | 868    | PCT-US95-08493-21 | Sequence 21, Appl  |

|    |       |     |      |   |                   |                   |
|----|-------|-----|------|---|-------------------|-------------------|
| 28 | 144.5 | 8.8 | 698  | 2 | US-08-602-725-36  | Sequence 36, Appl |
| 29 | 144.5 | 8.8 | 734  | 2 | US-08-389-459A-17 | Sequence 17, Appl |
| 30 | 144.5 | 8.8 | 734  | 3 | US-08-987-867A-17 | Sequence 17, Appl |
| 31 | 144.5 | 8.8 | 868  | 1 | US-08-374-834-1   | Sequence 1, Appli |
| 32 | 144.5 | 8.8 | 868  | 1 | US-08-644-271-1   | Sequence 1, Appli |
| 33 | 144   | 8.8 | 1651 | 4 | US-09-540-245A-18 | Sequence 18, Appl |
| 34 | 142.5 | 8.7 | 1260 | 4 | US-08-506-296B-21 | Sequence 21, Appl |
| 35 | 141   | 8.6 | 338  | 2 | US-08-414-657D-60 | Sequence 60, Appl |
| 36 | 141   | 8.6 | 642  | 1 | US-08-217-289-1   | Sequence 1, Appli |
| 37 | 141   | 8.6 | 1501 | 2 | US-08-447-464-3   | Sequence 3, Appli |
| 38 | 141   | 8.6 | 1501 | 2 | US-08-716-679-3   | Sequence 3, Appli |
| 39 | 139.5 | 8.5 | 612  | 2 | US-08-752-307B-11 | Sequence 11, Appl |
| 40 | 139.5 | 8.5 | 983  | 4 | US-09-412-554A-2  | Sequence 2, Appli |
| 41 | 139.5 | 8.5 | 1268 | 4 | US-08-506-296B-28 | Sequence 28, Appl |
| 42 | 139.5 | 8.5 | 1447 | 4 | US-09-041-886-25  | Sequence 25, Appl |
| 43 | 139.5 | 8.5 | 1447 | 5 | PCT-US94-05277-2  | Sequence 2, Appli |
| 44 | 139   | 8.5 | 310  | 2 | US-08-414-657D-45 | Sequence 45, Appl |
| 45 | 139   | 8.5 | 338  | 2 | US-08-414-657D-42 | Sequence 42, Appl |

## ALIGNMENTS

RESULT 1  
US-09-188-930-331  
Sequence 331, Application US/09188930A  
Patent No. 6150502  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Murison, James Greg  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
TITLE OF INVENTION: and Methods For their Use  
FILE REFERENCE: 11000.1011c1  
CURRENT APPLICATION NUMBER: US/09/188, 930A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 331  
LENGTH: 299  
TYPE: PRT  
ORGANISM: Human  
US-09-188-930-331

Query Match 25.4%, Score 415; DB 4; Length 299;  
Best Local Similarity 33.8%, Pred. No. 8.8e-34;  
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;

|    |     |   |
|----|-----|---|
| QY | 18  | FFLLILFFGCHIEAVNLKSSNRNPVHFEFSEVLSCLITTHSOTSPRIEMKKIDGCTTY 77     |
| DB | 15  | FTLLALICSLALGSLGVTHSSSEPVRIPENNPKLISC--AYSGFSSPREVMFKDGDTRL 72    |
| QY | 78  | VYFDKIKIGDLAGRTDVGKTSLRIMWTRTSATYRCEVALNDNRKKEVDETIELIYQV 137     |
| DB | 73  | VCYNKKITASTEDRY-TFLPTGIFTKSVTRDITGYTC-MSEEGNAGYGEKKVLLIV 130      |
| QY | 138 | KVPYPCVCRIPAAVPGYKATATLQCESEGYPRPHYSWYNDVPLPTDSRPNRPNFONSSFRV 197 |
| DB | 131 | PPSKRTVWIPSSATIGNNAVILCSQDSPPSEYTWFDGIVMPTNPKSTAFSSSVYL 190       |
| QY | 198 | NSEGTGLVFNAVHKDDSCQYICLANSNDGARCSQ--DMEEYDLNIIAGITGCVLVILV 256    |
| DB | 191 | NPTGELVFEDLSADPCEYCEARNGYCTPMTSNAVMEVVERVNGVIAVAIVLTLL 250        |
| QY | 257 | AVITMGICCAVRGCFISSKODGESYKSPGHGDNVYRTS--BERDPRHKSFPVY 310         |
| DB | 251 | GILVFGIIFAVSRGHFDRTKGTSSKK-----VITYSPARSRGEKOTSSFLV 299           |

RESULT 2





Patent No. 5712369  
GENERAL INFORMATION:  
APPLICANT: Old, Lloyd J.; Welt, Sydney; Rittler, Gerd;  
APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;  
APPLICANT: Calmel, B.; Ji, Hong; Burgess, Anthony W.;  
APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron  
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell  
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/597,495B  
FILING DATE: 02-Feb-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/511,876  
FILING DATE: 04-Aug-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5712369man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5316.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
FAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 319 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-597-495B-22

Query Match 14.8%; Score 242.5; DB 1; Length 319;  
Best Local Similarity 25.7%; Pred No. 2.2e-16;  
Matches 80; Conservative 49; Mismatches 123; Indels 59; Gaps 12;  
29 IEAVNLKSSNRPNVYHEFESVELSLIITHSOTS--DPRIEMKKIDGGOTTYYV---FDNK 83  
19 VDAISVETPQDVLRAISOGKSVTLPCYV-HTSTSSRGLIOWDKLLTHTHERVYIMFNSK 77  
84 --IQGL-----AGTDVFGKTSLRINWTRSDSAIRCEVVALNDRKDEITII 131  
78 NYIHGLYKNRYSISNNAOSD---ASTITIDLTWADNGTECSVSLMSDEGNTKRSV 133  
132 ELIVQKPTVPYCRIPAAPVPGKTAATLQCESGYPHPYSWYRNDV-----PLPTDSRA 186  
134 RLIVLVPSPKPEGIEGETIIGNNIOLTCOSKEGSPTPQYSKRYNIILNOEQPLAPASG 193  
187 NRPFONSSFRVNSEGTIVFNAVHKDDSGQYCIASNDAG-----AARCEGDMEVY 238  
194 QP-----VSLKNISDTSGYICTSSNEGTQFCNTTAVRSPSMVALY 238  
239 DLNIAIGTIGVLVLIIVAVITMGICCAVRRCGFISSKODG-----ESYSPKHKGVNTI 294  
239 ---VGIAGVVAALIIIGIT-IYCCCGKGDNDTEKEDARPNEAVEEPEQLRELSR 293  
295 RTSEEGDFRHK 305  
294 EREEDDYRQE 304

RESULT 6

US-09-068-051A-22  
Sequence 22, Application US/09068051A  
Patent No. 6291235  
GENERAL INFORMATION:  
APPLICANT: Old, Lloyd J.; Welt, Sydney; Rittler, Gerd;  
APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;  
APPLICANT: Calmel, B.; Ji, Hong; Burgess, Anthony W.;  
APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron  
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell  
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski LLP  
STREET: 666 Fifth Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/068,051A  
FILING DATE: 10-Dec-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/597,495  
FILING DATE: 02-Feb-1996  
APPLICATION NUMBER: 08/511,876  
FILING DATE: 04-Aug-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6291235man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5316.2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 318-3168  
FAX: (212) 752-5958  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 319 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 22  
US-09-068-051A-22

Query Match 14.8%; Score 242.5; DB 4; Length 319;  
Best Local Similarity 25.7%; Pred No. 2.2e-16;  
Matches 80; Conservative 49; Mismatches 123; Indels 59; Gaps 12;  
29 IEAVNLKSSNRPNVYHEFESVELSLIITHSOTS--DPRIEMKKIDGGOTTYYV---FDNK 83  
19 VDAISVETPQDVLRAISOGKSVTLPCYV-HTSTSSRGLIOWDKLLTHTHERVYIMFNSK 77  
84 --IQGL-----AGTDVFGKTSLRINWTRSDSAIRCEVVALNDRKDEITII 131  
78 NYIHGLYKNRYSISNNAOSD---ASTITIDLTWADNGTECSVSLMSDEGNTKRSV 133  
132 ELIVQKPTVPYCRIPAAPVPGKTAATLQCESGYPHPYSWYRNDV-----PLPTDSRA 186  
134 RLIVLVPSPKPEGIEGETIIGNNIOLTCOSKEGSPTPQYSKRYNIILNOEQPLAPASG 193  
187 NRPFONSSFRVNSEGTIVFNAVHKDDSGQYCIASNDAG-----AARCEGDMEVY 238  
194 QP-----VSLKNISDTSGYICTSSNEGTQFCNTTAVRSPSMVALY 238  
239 DLNIAIGTIGVLVLIIVAVITMGICCAVRRCGFISSKODG-----ESYSPKHKGVNTI 294  
239 ---VGIAGVVAALIIIGIT-IYCCCGKGDNDTEKEDARPNEAVEEPEQLRELSR 293  
295 RTSEEGDFRHK 305



ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,383B  
FILING DATE: 12-SEP-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,100  
FILING DATE: 13-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandagouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: DFN-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-928-383B-2

Query Match 10.6%; Score 173.5; DB 4; Length 365;  
Best Local Similarity 26.4%; Pred. No. 2.4e-09;  
Matches 70; Conservative 37; Mismatches 113; Indels 45; Gaps 12;

QY 47 ESVELSCITTHS-QTSDP-RIFM-----KKIQGQTTYYVFDKKGIOG----DIAGRTD 93  
DB 35 ETAYLPCKFTTSPEDQGLDIEMLISPADNCKVD--QVILISGKIXYDDYPPDLKGRVH 92  
QY 94 V-----FGKTSLRIMWYTRSDSAIYRCEVVALNDRKEVDEITIELIYQVKPVTFCRIP 147  
DB 93 FTSNDLKSGDASINTNTQLSDIGTYQCKV---KKAPGVANKKIHLYLVKPSGARCIVYD 149  
QY 148 AAVPVGKTATLQCESEGYPRPHYSWYR--NDVPLPTDSRANPRFONSSSFHVNSEGTGLV 205  
DB 150 GSEELISGFKICEPKESGLPLQYEMOKLSDQKMPSTSLA--EMTSSVISVKNMS----- 203  
QY 206 FNAVHKDSCGYCYCIASNDAGARCEGDMEYVDLNIAGIIGVLY-VLYVLAVITMGIC 264  
DB 204 -----SEYSGYTSCTVRRNRVGSDDCLRLNVVPSNKAAGLAIIGTLALALIGLIIF 258  
QY 265 CAVRRCFTISSKODGESYKSPGKHD 289  
DB 259 CCRK-----KRREKYEKEVHHND 276

RESULT 10  
US-08-979-424-3  
Sequence 3, Application US/08979424  
Patent No. 5942606  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,424  
FILING DATE: Filed Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0405 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 1946351  
US-08-979-424-3

Query Match 10.6%; Score 172.5; DB 2; Length 365;  
Best Local Similarity 25.9%; Pred. No. 3.1e-09;  
Matches 68; Conservative 38; Mismatches 116; Indels 41; Gaps 11;

QY 47 ESVELSCITTHS-QTSDP-RIFM-----KKIQGQTTYYVFDKKGIOG----DIAGRTD 93  
DB 35 ETAYLPCKFTTSPEDQGLDIEMLISPADNCKVD--QVILISGKIXYDDYPPDLKGRVH 92  
QY 94 V-----FGKTSLRIMWYTRSDSAIYRCEVVALNDRKEVDEITIELIYQVKPVTFCRIP 147  
DB 93 FTSNDLKSGDASINTNTQLSDIGTYQCKV---KKAPGVANKKIHLYLVKPSGARCIVYD 149  
QY 148 AAVPVGKTATLQCESEGYPRPHYSWYRNDVPLPTDSRANPRFONSSSFHVNSEGTGLVFN 207  
DB 150 GSEELISGFKICEPKESGLPLQYEMOK-----LSDQKMP-----TSLAEWMTSSVISVK 200  
QY 208 AVHKDSCGYCYCIASNDAGARCEGDMEYVDLNIAGIIGVLY-VLYVLAVITMGICCA 266  
DB 201 NASSEYSGYTSCTVRRNRVGSDDCLRLNVVPSNKAAGLAIIGTLALALIGLIIFCC 260  
QY 267 YRRCFTISSKODGESYKSPGKHD 289  
DB 261 RK-----KRREKYEKEVHHND 276

RESULT 11  
US-09-272-496-2  
Sequence 2, Application US/09272496  
Patent No. 6245966  
GENERAL INFORMATION:  
APPLICANT: Degregori, James  
TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes  
FILE REFERENCE: 90-98  
CURRENT APPLICATION NUMBER: US/09/272,496  
CURRENT FILING DATE: 1999-03-19  
EARLIER APPLICATION NUMBER: US 60/092782  
EARLIER FILING DATE: 1998-07-14  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 2  
LENGTH: 365  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-272-496-2



```

;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-986-485-2

```

|                       |                  |                  |            |              |
|-----------------------|------------------|------------------|------------|--------------|
| Query Match           | 10.2%;           | Score 166;       | DB 3;      | Length 1101; |
| Best Local Similarity | 22.8%;           | Pred. NO. 7e-08; |            |              |
| Matches 66;           | Conservative 44; | Mismatches 101;  | Indels 78; | Gaps 16;     |

```

OY 51 LSCJITHSOTDPIEMKKIODGOTTVYFENKIOGDLAGE-----TDVYKTSLR 101
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 626 LECATIGH--PNPDIANOK--DGITDP-----AARERAMHMPDDDFEITDYK 6711
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 102 IWNTRSDSAIYRCEVVALNDRKEVEDEITELIYQVRYTPVCRIP--AAVPGKATL 158
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 672 I-----DDAGCYSC--TAONSAGSISANATLTVE-----TPSLVLPLEDRVSVGTAL 720
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 159 OCOSEEGYPRHYSMYRNDVLPFRDSRANPRFQMSFHVNSFETGLFENAVHKHODSOXY 218
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    721 QC-KATGPPPRITWFGDRPLSTER-----HHLPDNOILLVQNVAVEDACRYT 770
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    219 CIASNDAGAACRCEGODEVYDLNIAIG-----GVLVLLILAVI--TWGICAY 267
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 771 CEMNLTGTERAHSQ-----LSVLPAAGCRKDGTOGIFLIAVSSIVLTSLWCIY 824
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 268 RRCGFISKQDEGSEYKSPGKHGY-----NYITSEGGDFRHKSSRYI 310
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 825 Q-----TRKSESEYVATNDEIVAPDPVSYL--SSQGTLSQDEQYV 865
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 14  
US-08-374-834-16  
; Sequence 16, Application US/08374834

GENERAL INFORMATION:  
APPLICANT: Valenzuela, et al.  
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road

```

1      COMPUTER READABLE FORM:
2
3      MEDIUM TYPE: Floppy disk
4
5      COMPUTER: IBM PC compatible
6
7      OPERATING SYSTEM: PC-DOS/MS-DOS
8
9      SOFTWARE: PatentIn Release #1.0, Version #1.30
10
11     CURRENT APPLICATION DATA:
12
13     APPLICATION NUMBER: US/08/374,834
14
15     FILING DATE: 19-JAN-1995

```

|                       |        |                  |       |                |
|-----------------------|--------|------------------|-------|----------------|
| Query Match           | 9.88;  | Score 160;       | DB 1; | Length 869;    |
| Best Local Similarity | 28.88; | Pred. No. 2e-07; |       |                |
| Matches               | 70;    | Conservative     | 23;   | Mismatches 82; |
|                       |        |                  |       | Indels 68;     |
|                       |        |                  |       | Gaps 11;       |

|    |     |   |     |
|----|-----|---|-----|
| Oy | 28  | MIEAVNLEKSSNRNPVHVEESESLS-----CITHSOTSP-----                  | 62  |
| Db | 1   | MRELVTNI-----PLVHILTLVAFSGHEKLPKAVITTPLETVDALVEEVAIFMCANESY   | 54  |
| Oy | 63  | --PRIEMWK---IQDGGTYVYFDPNNKIQDGLAGRTDVEGKTSLRJWNTSRDSAIYRCE   | 116 |
| Db | 55  | POPEISWTRNKLILKLEPDRSIREN---GOL-----LTLISVEDSDDGIIYCC-        | 99  |
| Oy | 117 | VVALNDKREVEDEITIELIYOKRPVTPYCRIPAAVY--GKTATIQCOESGSGYRPHHSWY  | 174 |
| Db | 100 | -TANGGCGAVESGCALOVKKP--KTIPIPIYKIIIEGLKAVLPC-TTGMNRPSPYSWI    | 155 |
| Oy | 175 | RNDVPLPTDSRANRPFONSSFHVNSSETGTLVFNAVHNDSDSGOYYCIAINDAGAARCGOD | 234 |
| Db | 156 | KGDSPLEKRENSRI-----AVLESOSLRIHNVQEDAGQYRCVAKNSLGTAYSRYVK      | 205 |
| Oy | 235 | MEV 237   |     |
| Db | 206 | LEV 208   |     |

RESULT 15  
US-08-644-271-29  
; Sequence 29, Application US/08644271

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COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fastseq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/644,271  
FILING DATE: 10-MAY-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:

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: INFORMATION FOR SEQ ID NO: 29:
:
: SEQUENCE CHARACTERISTICS:
:
:   LENGTH: 869 amino acids
:   TYPE: amino acid
:   STRANDEDNESS:
:
:   TOPOLOGY: unknown
:
:   MOLECULE TYPE: protein
:
:   US-08-644-271-29

```

Query Match 9.88; Score 160; DB 2; Length 869;

Best Local Similarity 28.8%; Pred. No. 2e-07;  
Matches 70; Conservative 23; Mismatches 82; Indels 68; Gaps 11;

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0Y      28  MIEAVNLKSSNRNVVHEEFSEVLS-----CIITHSOTSD-----62
Db      1  MRELVTNI-----PLVHLITLVAESGTEKLPKAVITTPLEIYDALVEEVAATMCVEST 54
0Y      63  --PRIEMWK-----IQDGQTVYVFDNKIQGDLAGRIVDFGKTSLRINWNTRSDSAIRCE 116
Db      55  P0PEISWTRNKLITKLPDTRISIREN---GOL-----LTLISVSDSDGIYCC- 99
0Y      117  VVALNDREVEDEITELIYQKVPVTPCIRIPAAVPV--GKTATLCOESGEGYRPHPSW 174
Db      100  -TANNQGAVESGALQVKKP--KITRPPINVKIIEGLKAVALPC-TTNGNRPSPYSWT 155
0Y      175  RNDVPLPTDSRANRPFONSSFHNVSEMTGLTVFNAAVHKHDDSGOYYCIASNDAGAARGOD 234
Db      156  KGDSPLRENSRI-----AVLESGSLRIHWQKEDAGQRCVAKNLSGTAYSRYVK 205
235  MEV 237
      :|
206  LEV 208

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Search completed: September 19, 2002, 17:33:15  
Job time: 233 sec







|    |     |  |     |
|----|-----|--|-----|
| Qy | 128 | EIVLEIVQVQVPPVPCVRPAAYVGMATTHCOESGHHPRPHYSWRNDVPLPPTSSRA                           | 187 |
|    |     | :  : |     |
| Db | 121 | EVAKKLIVLPSPKPYTNINPSAIGRAVITCSEQDQSPSEIYTWKDDIVAPTPNKST                           | 180 |
|    |     | :  :    |     |
| Qy | 188 | PRFRNSSFHLNSETGYLVE  | 206 |
|    |     | :  :    |     |
| Db | 181 | RAFSNSIVLNPPTGGLVE   | 199 |

## RESULT 5

```

US-08-597-495B-22
; Sequence 22, Application US/08597495B
; Patent No. 5712369
GENERAL INFORMATION:
APPLICANT: Old, Lloyd J.; Welt, Sydney; Rittner, Gerd;
APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
APPLICANT: Catmell, B.; Ji, Hong; Burgess, Anthony W.;
APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,495B
FILING DATE: 02-Feb-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5712369man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5316.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO.: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: linear
IS-08-597-495B-22

```

|                       |        |                    |        |                 |
|-----------------------|--------|--------------------|--------|-----------------|
| Query Match           | 14.0%; | Score 228.5;       | DB 1;  | Length 319;     |
| Best Local Similarity | 25.7%; | Pred. NO. 2.7e-15; |        |                 |
| Matches               | 79;    | Conservative       | 49;    | Mismatches 128; |
|                       |        |                    | Indels | 51;             |
|                       |        |                    | Gaps   | 14;             |

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OY      29  IGAUNLSSNRTPVJOEFSEYSLCII--TQSOTSDPIEMKKKIODEQTUVF---PUNK- 83
Dd      19  VDALSVEIPDQVYLAOSGKSTYLLPCTYHTSTSSREGLIQNDKLLHTTENVYIMPSNKN 78
OY      84  -TQGDL-----AGRAEILKTSFKIMWYTRDSALYRCEVYARNDRKEIDEIVELY 135
Dd      79  YIHELYKKNRYSINNAP--OSDASITTDQLTMDNGEYSECVSLMSDLBENTSRVLLY 137
OY      136  QVRPVTPTVCRRVPKAVPYVGKNAATLCQSESGHPRHRYHWYRNDV-----PLPTSRANPR 190
Dd      138  LVPPSKPBCGIEGFTITIGNNTQLTCSKESGPTQYGMKRYNLIINQPLAQRASQP-- 195
OY      191  RNSSEHLNSETGTVLFTAAVHKDQSGOYYCIASDNDAGSARCE--EDEMERYUNLNG---GIT 246

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Db 196 -----VSLNINISDTSGYIICTSSNEEGQPCNIIYVAVRSPMNAALYVIA 242
Qy 247 GCVLWLVLAIIITLGTICCAARRCYFIN--NKOG-----ESYKNPGPDGVNI--RTDE 298
Db 243 VGVAALAIITIIITIIYCCCC--RKQDNTEDKEDARPNNREAIIEP--PEQURELSRERE 297
Qy 299 EGDFRRHK 305
Db 298 EDDYRQE 304

```

## RESULT 6

US-09-068-051A-22  
: Sequence 22, Application US/09068051A  
: Patent No. 6291235  
: GENERAL INFORMATION:  
: APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;  
: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;  
: Catline, B.; Ji, Hong; Burgess, Anthony W.;  
: Heath, Joan K.; White, Sara J.; Johnstone, Cameron  
: TITLE OF INVENTION: Colon Cell And Colon Cancer Cell  
: Associated Nucleic Acid Molecules, Protein And Peptides  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Fulbright & Jaworski LLP  
: STREET: 666 Fifth Avenue  
: CITY: New York City  
: STATE: New York  
: COUNTRY: USA  
: ZIP: 10103  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
: COMPUTER: IBM PS/2  
: OPERATING SYSTEM: PC-DOS  
: SOFTWARE: Wordperfect  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/068,051A  
: FILING DATE: 10-Dec-1998  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/597,495  
: FILING DATE: 02-Feb-1996  
: APPLICATION NUMBER: 08/511,876  
: FILING DATE: 04-Aug-1995  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Hanson, No. 6291235man D.  
: REGISTRATION NUMBER: 30,946  
: REFERENCE/DOCKET NUMBER: LUD 5316.2  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (212) 318-3168  
: TELEFAX: (212) 752-5958  
: INFORMATION FOR SEQ ID NO: 22  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 319 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: SEQUENCE DESCRIPTION: SEQ ID NO: 22  
: US-09-068-051A-22

```

;          TOPOLOGY: linear
;          .
;          SEQUENCE DESCRIPTION: SEQ ID NO: 22
US-09-068-051A-22

```

| Query Match           | 14.0%            | Score 228.5;  | DB 4;                        | Length 319; |
|-----------------------|------------------|---|------------------------------|-------------|
| Best Local Similarity | 25.7%            | Pred. No. 2.7e-15;  |                              |             |
| Matches 79;           | Conservative 49; | Mismatches 128;   | Indels 51;                   | Gaps        |
| 0Y                    | 29               | IGAVNLKSSNFTPVQEFESVELSCII                                    | -TDSQTSDPRIENKKIODEQTYYVF--- | FDNK- 83    |
|                       |                  | : : : : : :   | : : : : : :                  | : : : : : : |
| Db                    | 19               | VDASIVETPQDVLPAASQGSVTLTCTYHTSSREGIOWDKLLTHTERVVIWIPESFNKN    |                              | 78          |
| 0Y                    | 84               | -IOGDL-----AGRAELIGKTSLKLTIMNTYRRRSLAYREGVANRKRKEIDETVELTV    |                              | 135         |
|                       |                  | : : : : : :   | : : : : : :                  | : : : : : : |
| Db                    | 79               | YIRBELTKNRKSTISNNAE-QSDASITITDOLTMADNGTYECSYSLSMDSEGTSSRVALLV |                              | 137         |
| 0Y                    | 136              | QVKEPVTVCVRPKAVPVGKMAITLHCQESGHPRHPSWYRNDV----                | PLPTDSRANPRF                 | 190         |





```

; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,424
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0405 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1946351
; US-08-979-424-3

Query Match          9.7%; Score 159.5; DB 2; Length 365;
Best Local Similarity 26.5%; Pred. No. 3.8e-08;
Matches 74; Conservative 35; Mismatches 123; Indels 47; Gaps 13;

QY 21 LLLFRGCLIGAVNLKSSNRTPVVOEF-----ESVELSCIITDS-QTSDP-RIEW----- 67
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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DB 3 LLLCFVLICGVDFARSLSTTPEEMIEKAKGETAYLPCKFTLSPEDOGFLDIEMLISPA 62
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 --KKIDEDTTFYFPDKKIOG-----DLGRAEIL-----GKTSIKIMVTRRDSALYRC 115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 63 DNQKV--DQYIILXSGDKITDDYPPDLKGRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 EVVARNDKREIDEIV--IELTVQVKRPVPCRVKAPVPGKMATLHCQSESGHPRPHYS 172
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 KV-----KAPGVANKKIHLYLVKPSGARCYVDGSEELGSDPKICEKREGSLPLQYE 174
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGLVFTAVHKDQSGQYCIASNDGASARCEE 232
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DB 175 WOK-----LSDSQKMP-----TSMLEMTSSVISVKNASSEYSGYCTVANNRNGSDQCL 225
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 233 QEMEVDNLNIGIIGVLY-VLAVLALITLGI-CCAYRR 269
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DB 226 RLNVVPPSKAGLIGLALIGLILFCCKRKR 264
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RESULT 12
US-09-272-496-2
; Sequence 2, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
; APPLICANT: Degreori, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes

```

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; FILE REFERENCE: 90-98
; CURRENT APPLICATION NUMBER: US/09/272,496
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/092782
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-272-496-2

Query Match          9.7%; Score 159.5; DB 4; Length 365;
Best Local Similarity 26.5%; Pred. No. 3.8e-08;
Matches 74; Conservative 35; Mismatches 123; Indels 47; Gaps 13;

QY 21 LLLFRGCLIGAVNLKSSNRTPVVOEF-----ESVELSCIITDS-QTSDP-RIEW----- 67
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 3 LLLCFVLICGVDFARSLSTTPEEMIEKAKGETAYLPCKFTLSPEDOGFLDIEMLISPA 62
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 68 --KKIDEDTTFYFPDKKIOG-----DLGRAEIL-----GKTSIKIMVTRRDSALYRC 115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 63 DNQKV--DQYIILXSGDKITDDYPPDLKGRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 EVVARNDKREIDEIV--IELTVQVKRPVPCRVKAPVPGKMATLHCQSESGHPRPHYS 172
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 KV-----KAPGVANKKIHLYLVKPSGARCYVDGSEELGSDPKICEKREGSLPLQYE 174
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGLVFTAVHKDQSGQYCIASNDGASARCEE 232
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 WOK-----LSDSQKMP-----TSMLEMTSSVISVKNASSEYSGYCTVANNRNGSDQCL 225
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 233 QEMEVDNLNIGIIGVLY-VLAVLALITLGI-CCAYRR 269
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 226 RLNVVPPSKAGLIGLALIGLILFCCKRKR 264
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-08-986-485-2
; Sequence 2, Application US/08986485
; Patent No. 6046030
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19462
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,485
; FILING DATE: 08-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,448
; FILING DATE: 22-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70264
; TELECOMMUNICATION INFORMATION:

```

RESULT 14  
US-08-752-307B-11  
Sequence 11, Application US/08752307B  
Patent No. 5952171  
GENERAL INFORMATION:  
APPLICANT: McCarthy, Sean A.  
APPLICANT: Gearing, David P.  
APPLICANT: Levinson, Douglas A.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,307B  
FILING DATE: 19-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

RESULT 15  
 US-08-506-2968-28  
 : Sequence 28, Application US/08506296B  
 : Patent No. 6313265  
 : GENERAL INFORMATION:  
 : APPLICANT: Phillips, Greg  
 : APPLICANT: Cunningham, Bruce A.  
 : APPLICANT: Crossin, Kathryn L.  
 : TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES  
 : TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE  
 : NUMBER OF SEQUENCES: 77  
 : CORRESPONDENCE ADDRESSES:  
 : ADDRESSEE: The Scripps Research Institute  
 : STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8  
 : CITY: La Jolla  
 : STATE: California  
 : COUNTRY: U.S.  
 : ZIP: 92037  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/506,296B  
 : FILING DATE: 24-JUL-1995  
 : CLASSIFICATION: 514  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Fitting, Thomas  
 : REGISTRATION NUMBER: 34,163  
 : REFERENCE/DOCKET NUMBER: TSRI 488.0  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (619) 554-2937  
 : TELEFAX: (619) 554-6312  
 : INFORMATION FOR SEQ ID NO: 28:  
 : SEQUENCE CHARACTERISTICS:

LENGTH: 1268 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-506-296B-28

Query Match 9.5%; Score 155.5; DB 4; Length 1268;  
Best Local Similarity 30.2%; Pred. No. 6.2e-07;  
Matches 60; Conservative 21; Mismatches 75; Indels 43; Gaps 10;

QY 40 TPVQEESEYE-----LSCIITDSQTSDPRIEMKKIODE-QTTYVFQNKIIGDLAGR 91  
Db 248 TPWGSTSNKVELRGNNVLLLECIAAGLPT--PVIRMIKEGGELPANRTFFEN----- 296  
QY 92 AEILGKTSLKIMWYTRDSALYRCEVVARNDKREIDETIVETLVQVKPVTVCRRVPKAVP 151  
Db 297 ----FKTKLIIDVSEADSGNYKC--TARNTLGSTHH-VISVYKAAPYWTAPRNLYLS 349  
152 VGRKATLHCQESRCHPRPHYSWYRNDVPL--PTD-SRANPRFRNSSFHLNSETGLVFT 207  
Db 350 PGEDGTLICR-ANGNPKPSISMLTNGVPIAIAPEDEPSR-----KVDGDTIIFS 396  
QY 208 AVHKDDSGQYICIASNDAG 226  
Db 397 AVOERSSAVYQCNAASNEYG 415

Search completed: September 19, 2002, 17:33:16  
Job time: 234 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:40:17 ; Search time 30.81 Seconds  
(without alignments)  
966.819 Million cell updates/sec

Title: US-09-524-531c-15  
Perfect score: 310  
Sequence: 1 MALRRPRLRLCARLPDFLL.....VNYIRDEGDFRHKSSFYI 310

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : PIR\_71:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description               |
|------------|-------|-------------|--------|-------|---------------------------|
| 1          | 8     | 2.6         | 290    | 2     | 168750 MHC class I lympho |
| 2          | 8     | 2.6         | 335    | 2     | A86406 probable RING zinc |
| 3          | 8     | 2.6         | 342    | 1     | HLHUC4 MHC class I histoc |
| 4          | 8     | 2.6         | 348    | 2     | E82933 type I restriction |
| 5          | 8     | 2.6         | 366    | 2     | JH0546 class I histocompa |
| 6          | 8     | 2.6         | 366    | 2     | JH0547 class I histocompa |
| 7          | 8     | 2.6         | 366    | 2     | JH0545 class I histocompa |
| 8          | 8     | 2.6         | 366    | 2     | 137078 HLA-C alpha chain  |
| 9          | 8     | 2.6         | 492    | 2     | A81013 probable membrane  |
| 10         | 8     | 2.6         | 784    | 2     | A86676 carbon starvation  |
| 11         | 7     | 2.3         | 77     | 2     | JC5645 lymphotoxin beta - |
| 12         | 7     | 2.3         | 113    | 2     | AH1748 lymphotoxin beta   |
| 13         | 7     | 2.3         | 171    | 2     | G70548 hypothetical prote |
| 14         | 7     | 2.3         | 172    | 2     | T08548 hypothetical prote |
| 15         | 7     | 2.3         | 173    | 2     | T01282 hypothetical prote |
| 16         | 7     | 2.3         | 173    | 2     | B90241 hypothetical prote |
| 17         | 7     | 2.3         | 173    | 2     | T25730 hypothetical prote |
| 18         | 7     | 2.3         | 177    | 2     | E85833 partial probable s |
| 19         | 7     | 2.3         | 177    | 2     | B90988 partial probable s |
| 20         | 7     | 2.3         | 208    | 2     | T03627 GTP-binding protei |
| 21         | 7     | 2.3         | 208    | 2     | T01588 GTP-binding protei |
| 22         | 7     | 2.3         | 211    | 2     | E86888 hypothetical prote |
| 23         | 7     | 2.3         | 214    | 2     | T47268 phosphatidylserine |
| 24         | 7     | 2.3         | 217    | 2     | T30446 occlusion-derived  |
| 25         | 7     | 2.3         | 242    | 2     | G84315 cobalt transport p |
| 26         | 7     | 2.3         | 244    | 2     | A46066 lymphotoxin beta   |
| 27         | 7     | 2.3         | 253    | 2     | T35883 transcription regu |
| 28         | 7     | 2.3         | 280    | 2     | PH0269 epidermal autoanti |
| 29         | 7     | 2.3         | 294    | 2     | H84023 phosphate ABC tran |

|    |   |     |     |   |                           |
|----|---|-----|-----|---|---------------------------|
| 30 | 7 | 2.3 | 297 | 2 | A81002 conserved hypothet |
| 31 | 7 | 2.3 | 297 | 2 | AB3037 hypothetical prote |
| 32 | 7 | 2.3 | 299 | 2 | A98249 nitrate transport  |
| 33 | 7 | 2.3 | 300 | 2 | A82017 probable lipoprote |
| 34 | 7 | 2.3 | 302 | 2 | B70471 heat shock protei  |
| 35 | 7 | 2.3 | 306 | 2 | I49139 lymphotoxin-beta - |
| 36 | 7 | 2.3 | 314 | 2 | G98193 sugar transport sy |
| 37 | 7 | 2.3 | 314 | 2 | AG3093 hypothetical prote |
| 38 | 7 | 2.3 | 324 | 2 | T27302 hypothetical prote |
| 39 | 7 | 2.3 | 333 | 2 | I38974 G protein-coupled  |
| 40 | 7 | 2.3 | 343 | 2 | H95879 probable sugar ABC |
| 41 | 7 | 2.3 | 346 | 2 | D75303 conserved hypothet |
| 42 | 7 | 2.3 | 362 | 2 | G75614 GDEF family prote  |
| 43 | 7 | 2.3 | 375 | 2 | T46378 hypothetical prote |
| 44 | 7 | 2.3 | 376 | 2 | F71815 hypothetical prote |
| 45 | 7 | 2.3 | 380 | 2 | E88421 protein R74.2 (imp |
| 46 | 7 | 2.3 | 382 | 2 | T24963 hypothetical prote |
| 47 | 7 | 2.3 | 391 | 2 | E72539 hypothetical prote |
| 48 | 7 | 2.3 | 392 | 1 | RWHUPD poliovirus recepto |
| 49 | 7 | 2.3 | 392 | 2 | B44194 poliovirus recepto |
| 50 | 7 | 2.3 | 400 | 2 | T24258 poliovirus recepto |
| 51 | 7 | 2.3 | 402 | 2 | T04348 endospore specific |
| 52 | 7 | 2.3 | 402 | 2 | G83367 hypothetical prote |
| 53 | 7 | 2.3 | 403 | 1 | GRECY tyrosine-specific   |
| 54 | 7 | 2.3 | 403 | 2 | G90955 tyrosine-specific  |
| 55 | 7 | 2.3 | 403 | 2 | D85804 tyrosine-specific  |
| 56 | 7 | 2.3 | 417 | 1 | RWHUPA poliovirus recepto |
| 57 | 7 | 2.3 | 417 | 2 | A44194 poliovirus recepto |
| 58 | 7 | 2.3 | 420 | 2 | T36532 probable membrane  |
| 59 | 7 | 2.3 | 421 | 2 | H86217 protein T2767.16 [ |
| 60 | 7 | 2.3 | 431 | 2 | D81282 probable efflux pr |
| 61 | 7 | 2.3 | 437 | 2 | AE1849 proton/sodium-glut |
| 62 | 7 | 2.3 | 454 | 2 | JC4616 apyrase (EC 3.6.1. |
| 63 | 7 | 2.3 | 463 | 2 | D84065 glucose-1-phosphat |
| 64 | 7 | 2.3 | 481 | 2 | S69808 lincomycin resista |
| 65 | 7 | 2.3 | 490 | 2 | A96556 probable tRNA-guan |
| 66 | 7 | 2.3 | 491 | 1 | O4R8PC cytochrome P450 2B |
| 67 | 7 | 2.3 | 491 | 2 | S31277 cytochrome P450 2B |
| 68 | 7 | 2.3 | 491 | 2 | S31278 cytochrome P450 2B |
| 69 | 7 | 2.3 | 491 | 2 | S35666 cytochrome P450 2B |
| 70 | 7 | 2.3 | 503 | 2 | E83450 probable MFS trans |
| 71 | 7 | 2.3 | 504 | 2 | E87628 hypothetical prote |
| 72 | 7 | 2.3 | 523 | 2 | B95922 hypothetical nucle |
| 73 | 7 | 2.3 | 524 | 2 | A31318 glucose transporte |
| 74 | 7 | 2.3 | 530 | 2 | C95268 probable ABC trans |
| 75 | 7 | 2.3 | 558 | 2 | B87098 conserved hypothet |

ALIGNMENTS

RESULT 1  
MHC class I lymphocyte antigen - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 21-Jan-2000  
C:Accession: 168750  
R:Polnla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.  
Immunogenetics 29, 297-307, 1989  
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-  
A:Reference number: I54457; MUID:89233295  
A:Accession: 168750  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-290 <RES>  
A:Cross-references: GB:M28207; NID:9576478; PIDN:AAA53259.1; PID:9576479  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:144-209/Domain: immunoglobulin homology <IMM>

Query Match 2.6%; Score 8; DB 2; Length 290;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 249 VLVLAVL 256  
 Db 241 VLVLAVL 248

## RESULT 2

probable RING zinc finger protein [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: AB6406  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzilli, R.; M.; Rooney, T.; Rowley, D.; Sakano, H.; Scheraga, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: AB6141; MUID:21016719  
 A:Accession: AB6406  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-336 <STO>  
 A:Cross-references: GB:AE005172; NID:g11024872; PIDN:AAQ26956.1; GSPDB:GN00141  
 C:Genetics:  
 A:Map position: 1

Query Match 2.6%; Score 8; DB 2; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 LVLVLAVL 257  
 Db 28 LVLVLAVL 35

## RESULT 3

H1HUC4  
 MHC class I histocompatibility antigen HLA-C4 alpha chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 22-Jun-1999  
 C:Accession: A24512  
 A:Authors: Kress, M.; Khoury, G.; Jay, G.  
 A:Title: Chem. 260, 13414-13423, 1985  
 A:Reference number: A92500; MUID:86033791  
 A:Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonucleotide.  
 A:Accession: A24512  
 A:Molecule type: DNA  
 A:Residues: 1-342 <DAV>  
 A:Cross-references: GB:M11886; NID:g184173; PIDN:AAA52665.1; PID:g386777  
 C:Genetics:  
 A:Gene: GDB:HLA-C  
 A:Cross-references: GDB:119311; OMIM:142840  
 A:Map position: 6p21.3-6p21.3  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen  
 F:196-261/Domain: immunoglobulin homology <IMM>  
 F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.6%; Score 8; DB 1; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 6.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 VLVLAVL 256  
 Db 253 VLVLAVL 300

RESULT 4  
 E82933  
 type I restriction enzyme M protein, truncated homolog U0098 [imported] - Ureaplasma urealyticum  
 C:Species: Ureaplasma urealyticum  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C:Accession: E82933  
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Helner, C.R.; Chen, E.Y.; Cassell, G.H.  
 submitted to Genbank, February 2000  
 A:Description: The complete sequence of Ureaplasma urealyticum. Alternate views of a  
 A:Reference number: AB2870  
 A:Accession: E82933  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-348 <GLA>  
 A:Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30504.1; GSPDB:GN  
 A:Experimental source: serovar 3; biovar 1  
 C:Genetics:  
 A:Gene: hsdM-1; U0098  
 A:Genetic code: SGC3

Query Match 2.6%; Score 8; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 RKEIDETV 130  
 Db 336 RKEIDETV 343

## RESULT 5

JH0546  
 class I histocompatibility antigen Gogo-C0202 heavy chain precursor - lowland gorilla  
 C:Species: Gorilla gorilla gorilla (lowland gorilla)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
 C:Accession: JH0546  
 R:Rawlton, D.A.; Warren, E.; Taylor, P.; Parham, P.  
 J. Exp. Med. 174, 1491-1509, 1991  
 A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human.  
 A:Reference number: JH0534; MUID:92078860  
 A:Accession: JH0546  
 A:Molecule type: DNA  
 A:Residues: 1-366 <LAW>  
 A:Cross-references: EMBL:X60249; NID:g22882; PIDN:CAA42801.1; PID:g22883  
 A:Experimental source: EBV-transformed B cell  
 C:Genetics:  
 A:Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 C:Keywords: transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0202 #status  
 F:25-114/Domain: alpha-1 <AL1>  
 F:115-206/Domain: alpha-2 <AL2>  
 F:207-298/Domain: alpha-3 <AL3>  
 F:220-285/Domain: immunoglobulin homology <IMM>  
 F:299-366/Domain: intracellular #status predicted <INT>

Query Match 2.6%; Score 8; DB 2; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 7.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 VLVLAVL 256  
 Db 317 VLVLAVL 324

## RESULT 6

JH0547  
 class I histocompatibility antigen Gogo-C0203 heavy chain precursor - lowland gorilla  
 C:Species: Gorilla gorilla gorilla (lowland gorilla)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:46:24 : Search time 17.64 Seconds  
(without alignments)  
680.446 Million cell updates/sec

Title: US-09-524-531c-15  
Perfect score: 310  
Sequence: 1 MALRRPRLRLCARLPDFLL.....VNYIRDEGDFRHKSSFYI 310

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Length | ID    | Description |
|------------|-------|--------------|-------|-------------|
| 1          | 8     | 2.6          | 80 1  | TX3A_PHONI  |
| 2          | 8     | 2.6          | 342 1 | ICXX_HUMAN  |
| 3          | 8     | 2.6          | 366 1 | IC02_GORGO  |
| 4          | 8     | 2.6          | 366 1 | IC03_GORGO  |
| 5          | 8     | 2.6          | 366 1 | IC04_GORGO  |
| 6          | 8     | 2.6          | 366 1 | IC11_HUMAN  |
| 7          | 8     | 2.6          | 435 1 | YGIR_SALTY  |
| 8          | 7     | 2.3          | 224 1 | XLRI_MOUSE  |
| 9          | 7     | 2.3          | 244 1 | TNFC_MOUSE  |
| 10         | 7     | 2.3          | 302 1 | HTPX_AQUAE  |
| 11         | 7     | 2.3          | 306 1 | TNFC_MOUSE  |
| 12         | 7     | 2.3          | 333 1 | GPR8_HUMAN  |
| 13         | 7     | 2.3          | 343 1 | HMD_MITO    |
| 14         | 7     | 2.3          | 403 1 | TYRP_ECOLI  |
| 15         | 7     | 2.3          | 417 1 | PVR_CERAE   |
| 16         | 7     | 2.3          | 417 1 | PVR_HUMAN   |
| 17         | 7     | 2.3          | 454 1 | APY_SOLTU   |
| 18         | 7     | 2.3          | 481 1 | LMRA_STRLN  |
| 19         | 7     | 2.3          | 491 1 | CPB4_RABIT  |
| 20         | 7     | 2.3          | 491 1 | CPB5_RABIT  |
| 21         | 7     | 2.3          | 524 1 | GT22_HUMAN  |
| 22         | 7     | 2.3          | 595 1 | FE2P_ARCFU  |
| 23         | 7     | 2.3          | 617 1 | PXS1_PSEAE  |
| 24         | 7     | 2.3          | 643 1 | PST_HUMAN   |
| 25         | 7     | 2.3          | 643 1 | PST_RAT     |
| 26         | 7     | 2.3          | 688 1 | PYS2_PSEAE  |
| 27         | 7     | 2.3          | 697 1 | TGLC_CHICK  |
| 28         | 7     | 2.3          | 721 1 | VJIV_ECOLI  |
| 29         | 7     | 2.3          | 758 1 | SC18_YEAST  |
| 30         | 7     | 2.3          | 840 1 | CC16_YEAST  |
| 31         | 7     | 2.3          | 961 1 | SCA4_RICE   |
| 32         | 7     | 2.3          | 987 1 | K6P1_CANAL  |
| 33         | 7     | 2.3          | 991 1 | SCA4_RICSI  |

|    |   |     |        |            |                     |
|----|---|-----|--------|------------|---------------------|
| 34 | 7 | 2.3 | 1011 1 | SCA4_RICAF | 09aj83 rickettsia   |
| 35 | 7 | 2.3 | 1011 1 | SCA4_RICIN | 09aj82 rickettsia   |
| 36 | 7 | 2.3 | 1012 1 | SCA4_RICEL | 09aj80 rickettsia   |
| 37 | 7 | 2.3 | 1013 1 | SCA4_RICHL | 09aj81 rickettsia   |
| 38 | 7 | 2.3 | 1018 1 | SCA4_RICJA | 09aj79 rickettsia   |
| 39 | 7 | 2.3 | 1022 1 | SCA4_RICN  | 052658 rickettsia   |
| 40 | 7 | 2.3 | 1053 1 | ITR3_MOUSE | 062470 mus musculus |
| 41 | 7 | 2.3 | 1066 1 | ITR3_CRISP | 171852 rickettsiae  |
| 42 | 7 | 2.3 | 1066 1 | ITR3_HUMAN | P26006 homo sapien  |
| 43 | 7 | 2.3 | 1105 1 | YGE_ECOLI  | P38097 escherichia  |
| 44 | 7 | 2.3 | 1169 1 | EX5B_BORBU | 051578 borrelia bu  |
| 45 | 7 | 2.3 | 1234 1 | YXK5_CAEEL | P34578 caenorhabdi  |
| 46 | 7 | 2.3 | 1684 1 | PLE1_HUMAN | 015149 homo sapien  |
| 47 | 7 | 2.3 | 5065 1 | EPPL_HUMAN | P58107 homo sapien  |
| 48 | 7 | 1.9 | 38 1   | CNS3_NORGO | P15534 notocodatus  |
| 49 | 6 | 1.9 | 46 1   | LHAI_ECTHA | P80100 ectothiorho  |
| 50 | 6 | 1.9 | 57 1   | ANDP_DROME | P21663 drosophila   |
| 51 | 6 | 1.9 | 57 1   | Y160_ARCFU | 028419 archaeoglob  |
| 52 | 6 | 1.9 | 61 1   | RS14_MYCGA | 052345 mycoplasma   |
| 53 | 6 | 1.9 | 64 1   | YDPE_SCHPO | 014211 schizosacch  |
| 54 | 6 | 1.9 | 76 1   | SRR_SOYBN  | 007502 glycine max  |
| 55 | 6 | 1.9 | 76 1   | SEC6_BACSU | 032233 bacillus su  |
| 56 | 6 | 1.9 | 82 1   | TX32_PHONI | 076201 phoneutria   |
| 57 | 6 | 1.9 | 83 1   | TX31_PHONI | 076200 phoneutria   |
| 58 | 6 | 1.9 | 86 1   | PRHP_STRMU | P45596 streptococc  |
| 59 | 6 | 1.9 | 87 1   | PRHP_BACBD | 09x842 bacillus ha  |
| 60 | 6 | 1.9 | 87 1   | PRHP_STRBO | 09x848 streptococc  |
| 61 | 6 | 1.9 | 87 1   | PRHP_STRSL | P24366 streptococc  |
| 62 | 6 | 1.9 | 94 1   | YE23_HAEIN | P44194 haemophilus  |
| 63 | 6 | 1.9 | 96 1   | FER1_AQUAE | 067065 aquifex aeo  |
| 64 | 6 | 1.9 | 99 1   | Y010_BPHPI | P51712 bacterioph   |
| 65 | 6 | 1.9 | 102 1  | KCRB_PIG   | 029594 sus scrofa   |
| 66 | 6 | 1.9 | 109 1  | V42_BPT3   | P20316 bacterioph   |
| 67 | 6 | 1.9 | 115 1  | NRG4_MOUSE | Q9wlc4 mus musculu  |
| 68 | 6 | 1.9 | 115 1  | TN11_RABIT | P41540 oryctolagus  |
| 69 | 6 | 1.9 | 118 1  | YKD7_YEAST | P32858 saccharomyc  |
| 70 | 6 | 1.9 | 119 1  | B2MG_HUMAN | P01884 homo sapien  |
| 71 | 6 | 1.9 | 119 1  | B2MG_PONPY | P16213 pongo pygma  |
| 72 | 6 | 1.9 | 123 1  | Y055_MYCGE | P47301 mycoplasma   |
| 73 | 6 | 1.9 | 125 1  | FRDD_MYCTU | Q10763 mycobacteri  |
| 74 | 6 | 1.9 | 130 1  | DHSC_PARDE | Q59659 paracoccus   |
| 75 | 6 | 1.9 | 130 1  | KV5G_MOUSE | P01639 mus musculu  |

#### ALIGNMENTS

RESULT 1  
TX3A\_PHONI STANDARD: PRT: 80 AA.  
AC P81793;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DE 01-MAR-2002 (Rel. 41, Last annotation update)  
OS Neurotoxin Pn3a precursor.  
OC Phoneutria nigriverter (Brazilian armed spider).  
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
CC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.  
OX NCBI\_Taxid:6918;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Venom gland.  
RA MEDLINE-99053416; PubMed-9839681;  
RA Kalapothakis E., Penaforte C.L., Ileano R.M., Cruz J.S., Prado V.F.,  
RA Cordeliro M.N., Diniz C.R., Romano-Silva M.A., Prado M.A.M.,  
RT "Cloning", cDNA sequence analysis and patch clamp studies of a toxin  
RT from the venom of the armed spider (Phoneutria nigriverter).";  
RL Toxicon 36:1971-1980(1998).  
CC -1- FUNCTION: ANTAGONIST OF L-TYPE CALCIUM CHANNELS (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Produced by the venomous gland.  
CC -1- SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY.

DR InterPro: IPR004169; spider toxin.  
 DR Pfam: PF02819; spider toxin; 1.  
 KW Calcium channel inhibitor; Toxin; Neurotoxin; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT PROPEP 22 37 POTENTIAL.  
 FT CHAIN 38 71 NEUROTOXIN PN3A.  
 FT PROPEP 72 80 POTENTIAL.  
 SQ SEQUENCE 80 AA; 8937 MW; B5BF209257EB6793 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 0.98;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 256 LALITLGI 263  
 DB 12 LALITLGI 19

LT 2  
 ID HUMAN STANDARD; PRT: 342 AA.  
 AC P10321;  
 DT 01-MAR-1989 (Rel. 10; Created)  
 DT 01-MAR-1989 (Rel. 10; Last sequence update)  
 DT 16-OCT-2001 (Rel. 40; Last annotation update)  
 DE HLA class I histocompatibility antigen, C-4 alpha chain.  
 GN HLA-C OR HLA-C.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86033791; Pubmed=3863816;  
 RA Davidson W.F., Kress M., Khoury G., Jay G.;  
 RT "Comparison of HLA class I gene sequences. Derivation of  
 RT locus-specific oligonucleotide probes specific for HLA-A, HLA-B, and  
 RT HLA-C genes."  
 RL J. Biol. Chem. 260:13414-13423(1985).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC -----  
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 CC -----  
 DR EMBL: M1886; AAA52665.1; -  
 DR PIR: A24512; HLHUC4.  
 DR HSSP: P30685; 1A9B.  
 DR MIM: 142840; -  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR001039; MHC\_I.  
 DR Pfam: PF00047; Ig\_1.  
 DR Pfam: PF00129; MHC\_I; 1.  
 DR ProDom: PD000050; MHC\_I; 1.  
 DR SMART: SM00407; IGc1; 1.  
 DR PROSITE: PS00290; IG\_MHC; FALSE\_NEG.  
 KW MHC I; Transmembrane; Glycoprotein.  
 FT DOMAIN 25 90 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 91 182 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 183 274 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 275 284 CONNECTING PEPTIDE.  
 FT TRANSMEM 285 309  
 FT DOMAIN 310 342  
 FT CARBOHYD 86 86 CYTOPLASMIC TAIL.  
 N-LINKED (GLCNAC. .) (BY SIMILARITY).

FT DISULFID 164 203 BY SIMILARITY.  
 SQ SEQUENCE 342 AA; 38082 MW; 22C39A6D84C05D09 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 3.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 VLVVLAVL 256  
 DB 293 VLVVLAVL 300

RESULT 3  
 ID 1C02\_GORGO STANDARD; PRT: 366 AA.  
 AC P30385;  
 DT 01-APR-1993 (Rel. 25; Created)  
 DT 01-APR-1993 (Rel. 25; Last sequence update)  
 DT 01-NOV-1997 (Rel. 35; Last annotation update)  
 DE Class I histocompatibility antigen, GOGC-C0201 alpha chain precursor.  
 OS Gorilla gorilla gorilla (Lowland gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.  
 OX NCBI\_TaxID=9595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92078860; Pubmed=1744581;  
 RA Lawlor D.A., Warren E., Taylor P., Parham P.;  
 RT "Gorilla class I major histocompatibility complex alleles: comparison  
 RT to human and chimpanzee class I."  
 RL J. Exp. Med. 174:1491-1509(1991).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC -----  
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 CC -----  
 DR EMBL: X60251; CAA42803.1; -  
 DR PIR: JH0545; JH0545.  
 DR HSSP: P30685; 1A9B.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR001039; MHC\_I.  
 DR Pfam: PF00047; Ig\_1.  
 DR Pfam: PF00129; MHC\_I; 1.  
 DR ProDom: PD000050; MHC\_I; 1.  
 DR SMART: SM00407; IGc1; 1.  
 DR PROSITE: PS00290; IG\_MHC; FALSE\_NEG.  
 KW MHC I; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 366  
 FT DOMAIN 25 114  
 FT DOMAIN 115 206  
 FT DOMAIN 207 298  
 FT DOMAIN 299 308  
 FT TRANSMEM 309 333  
 FT DOMAIN 334 366  
 FT DISULFID 125 188  
 FT DISULFID 227 283  
 FT CARBOHYD 110 110  
 SQ SEQUENCE 366 AA; 40954 MW; 05E159364C769C5 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 366;

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:44:45 : Search time 48.09 Seconds  
(without alignments)  
1115.168 Million cell updates/sec

Title: US-09-524-531c-15  
Perfect score: 310  
Sequence: 1 MALRRPRLRCARLPDFL.....VNIITDEGDFRHKSSFYI 310

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

SPREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 310   | 100.0       | 310    | 4     | 09BX67      |
| 2          | 208   | 67.1        | 309    | 4     | 09BFL1      |
| 3          | 32    | 10.3        | 310    | 11    | 09DB87      |
| 4          | 28    | 9.0         | 310    | 11    | 09EPK4      |
| 5          | 28    | 9.0         | 310    | 11    | 09D1M9      |
| 6          | 8     | 2.6         | 39     | 7     | 09TWT2      |
| 7          | 8     | 2.6         | 80     | 5     | P81793      |
| 8          | 8     | 2.6         | 125    | 11    | 09CS62      |
| 9          | 8     | 2.6         | 233    | 10    | 09LR49      |
| 10         | 8     | 2.6         | 246    | 5     | 0966C0      |
| 11         | 8     | 2.6         | 290    | 7     | 029990      |
| 12         | 8     | 2.6         | 294    | 16    | 098E09      |
| 13         | 8     | 2.6         | 309    | 8     | 09NAY9      |
| 14         | 8     | 2.6         | 313    | 7     | 09MT31      |
| 15         | 8     | 2.6         | 322    | 2     | 09RP17      |
| 16         | 8     | 2.6         | 336    | 10    | 09C7E9      |

|    |   |     |      |    |        |                    |
|----|---|-----|------|----|--------|--------------------|
| 17 | 8 | 2.6 | 338  | 7  | 09MXL5 | 09mx15 pan troglod |
| 18 | 8 | 2.6 | 348  | 7  | 09MMJ9 | 09mw19 gorilla gor |
| 19 | 8 | 2.6 | 348  | 16 | 09PR46 | 09pr46 ureaplasma  |
| 20 | 8 | 2.6 | 363  | 7  | 095HC2 | 095hc2 homo sapien |
| 21 | 8 | 2.6 | 365  | 7  | 09XRX8 | 09xrx8 pongo pygma |
| 22 | 8 | 2.6 | 365  | 7  | 09XRX7 | 09xrx7 pongo pygma |
| 23 | 8 | 2.6 | 365  | 7  | 09XRX4 | 09mx94 pan troglod |
| 24 | 8 | 2.6 | 366  | 6  | 046684 | 046684 pan troglod |
| 25 | 8 | 2.6 | 366  | 7  | 09PPL2 | 09tpl2 pan troglod |
| 26 | 8 | 2.6 | 366  | 7  | 09MXD2 | 09mx02 pan troglod |
| 27 | 8 | 2.6 | 366  | 7  | 095603 | 095603 homo sapien |
| 28 | 8 | 2.6 | 366  | 7  | 095463 | 095463 homo sapien |
| 29 | 8 | 2.6 | 366  | 7  | 029865 | 029865 homo sapien |
| 30 | 8 | 2.6 | 366  | 7  | 078083 | 078083 homo sapien |
| 31 | 8 | 2.6 | 366  | 7  | 09R0P9 | 09r0p9 homo sapien |
| 32 | 8 | 2.6 | 366  | 7  | 029652 | 029652 homo sapien |
| 33 | 8 | 2.6 | 366  | 7  | 019617 | 019617 homo sapien |
| 34 | 8 | 2.6 | 784  | 16 | 09CIF4 | 09cif4 lactococcus |
| 35 | 8 | 2.6 | 1290 | 13 | 09W6E1 | 09w6e1 gallus gall |
| 36 | 7 | 2.3 | 77   | 4  | P78370 | P78370 homo sapien |
| 37 | 7 | 2.3 | 85   | 12 | 099GX8 | 099gx8 helicoverp  |
| 38 | 7 | 2.3 | 113  | 16 | 0928J9 | 0928j9 listeria in |
| 39 | 7 | 2.3 | 146  | 17 | 0973F7 | 0973f7 sulfolobus  |
| 40 | 7 | 2.3 | 158  | 2  | 09EWB3 | 09ewb3 streptomyce |
| 41 | 7 | 2.3 | 161  | 2  | 09FBR8 | 09fbr8 streptomyce |
| 42 | 7 | 2.3 | 171  | 16 | 006422 | 006422 mycobacteri |
| 43 | 7 | 2.3 | 172  | 10 | 09S208 | 09sx08 arabidopsis |
| 44 | 7 | 2.3 | 173  | 5  | 022966 | 022966 caenorhabdi |
| 45 | 7 | 2.3 | 173  | 10 | 064567 | 064567 arabidopsis |
| 46 | 7 | 2.3 | 173  | 17 | 0972K3 | 0972k3 sulfolobus  |
| 47 | 7 | 2.3 | 177  | 16 | 0931Y0 | 0931y0 staphylococ |
| 48 | 7 | 2.3 | 179  | 2  | 09RKC2 | 09rk02 streptomyce |
| 49 | 7 | 2.3 | 191  | 10 | 09XHM2 | 09xhm2 medicago tr |
| 50 | 7 | 2.3 | 202  | 6  | 09RUP5 | 09ruf5 ceropithec  |
| 51 | 7 | 2.3 | 202  | 6  | 09TUP4 | 09tuf4 prothecus   |
| 52 | 7 | 2.3 | 208  | 10 | 080501 | 080501 arabidopsis |
| 53 | 7 | 2.3 | 208  | 10 | 040525 | 040525 nicotiana t |
| 54 | 7 | 2.3 | 211  | 16 | 09CDV2 | 09cdv2 lactococcus |
| 55 | 7 | 2.3 | 214  | 2  | 032618 | 032618 helicobacte |
| 56 | 7 | 2.3 | 214  | 6  | 062722 | 062722 oryctolagus |
| 57 | 7 | 2.3 | 217  | 12 | 09YMN1 | 09ymn1 lymantria d |
| 58 | 7 | 2.3 | 224  | 11 | 09R1M6 | 09r1m6 mus musculu |
| 59 | 7 | 2.3 | 227  | 12 | 091BE2 | 091be2 spodoptera  |
| 60 | 7 | 2.3 | 242  | 17 | 09HPH6 | 09hph6 halobacteri |
| 61 | 7 | 2.3 | 242  | 17 | 096XA1 | 096xa1 sulfolobus  |
| 62 | 7 | 2.3 | 247  | 4  | 075192 | 075192 homo sapien |
| 63 | 7 | 2.3 | 255  | 2  | 050521 | 050521 streptomyce |
| 64 | 7 | 2.3 | 267  | 3  | 09Y7B2 | 09y7b2 emeticella  |
| 65 | 7 | 2.3 | 275  | 16 | 092NE9 | 092ne9 rhizobium m |
| 66 | 7 | 2.3 | 277  | 11 | P70361 | P70361 mus musculu |
| 67 | 7 | 2.3 | 280  | 9  | 09XJ89 | 09xj89 bacterioph  |
| 68 | 7 | 2.3 | 286  | 2  | 09EM05 | 09em05 streptomyce |
| 69 | 7 | 2.3 | 292  | 10 | 09SE74 | 09se74 brassica ca |
| 70 | 7 | 2.3 | 294  | 10 | 09SE75 | 09se75 brassica ol |
| 71 | 7 | 2.3 | 294  | 16 | 09RBL4 | 09rbl4 bacillus ha |
| 72 | 7 | 2.3 | 297  | 16 | 09JXB2 | 09jxb2 neisseria m |
| 73 | 7 | 2.3 | 300  | 16 | 09JMV3 | 09jmv3 neisseria m |
| 74 | 7 | 2.3 | 306  | 16 | 092K19 | 092k19 rhizobium m |
| 75 | 7 | 2.3 | 310  | 11 | 09JMI1 | 09jmi1 marmota mon |

#### ALIGNMENTS

RESULT 1  
ID 09BX67  
AC 09BX67;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE JUNCTIONAL ADHESION MOLECULE 3 PRECURSOR (JUNCTIONAL ADHESION MOLECULE-2).

JAM-2.  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxId=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRIN;  
 RA Cunningham S.A., Arrate M.P., Tran T.M.;  
 RT "Cloning of Human Junctional Adhesion Molecule 3."  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Aurand-Lions M.A., Johnson-Ieger C., Mong C., Dupasquier L.;  
 RT "Heterogeneity of endothelial junctions is reflected by differential  
 expression and specific subcellular localization of the three JAM  
 family members."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RA Aurand-Lions M.A., Johnson-Ieger C., Lamagna C., Ozaki H., Kita T.;  
 RT "Junctional adhesion molecules (JAMs) and interendothelial  
 junctions."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF356518; AAK27221.1; -  
 DR EMBL; AJ344431; CAC69845.1; -  
 DR InterPro: IPR003598; 1g\_c2.  
 DR InterPro: IPR003600; 1g\_1ike.  
 DR InterPro: IPR003066; 1g\_1MC.  
 DR Pfam: PF00047; 1g\_2.  
 DR SMART: SM00409; 1g\_2.  
 DR SMART: SM00408; 1gc2; 2.  
 DR SMART: SM00410; 1g\_1like; 1.  
 DR Immunoglobulin domain; Signal.  
 KW SIGNAL  
 FT 1 30 POTENTIAL.  
 SQ SEQUENCE 310 AA; 35020 MW; CE39ADF3EALDAB9 CRC64;

Query Match 100.0%; Score 310; DB 4; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFSEVLSCTITDSQT 60  
 DB 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFSEVLSCTITDSQT 60  
 QY 61 SDRRIEMKKIQDEQTYVFFDNKIQDLAGRAEILKTSKIMNVTFRDSALYRCEVVAR 120  
 DB 61 SDRRIEMKKIQDEQTYVFFDNKIQDLAGRAEILKTSKIMNVTFRDSALYRCEVVAR 120  
 QY 121 NDRKEIDEIVIELTVQVKPTVPCRYPKAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 180  
 DB 121 NDRKEIDEIVIELTVQVKPTVPCRYPKAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 180  
 QY 181 PDSRANPRFRNSSFHLNSETGLVFTAVHKDMSGQYCIASNDASARCEQEMEYDYL 240  
 DB 181 PDSRANPRFRNSSFHLNSETGLVFTAVHKDMSGQYCIASNDASARCEQEMEYDYL 240  
 QY 241 NIGGIIGVLYLAVLALITLIGICAYRGRYFINNKQDESEYKPNKPGVNIYRTDEEG 300  
 DB 241 NIGGIIGVLYLAVLALITLIGICAYRGRYFINNKQDESEYKPNKPGVNIYRTDEEG 300  
 QY 301 DFRHKSFEVI 310  
 DB 301 DFRHKSFEVI 310  
 RESULT 2  
 ID 096FL1 PRELIMINARY; PRT; 309 AA.  
 AC 096FL1  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE UNKNOWN (PROTEIN FOR IMAGE:3875338) (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxId=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=EYE, AND RETINOBLASTOMA;  
 RA Strausberg R.;  
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC010690; AAH10690.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;

Query Match 67.1%; Score 208; DB 4; Length 309;  
 Best Local Similarity 99.7%; Pred. No. 2.2e-204;  
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFSEVLSCTITDSQT 61  
 DB 1 ALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFSEVLSCTITDSQT 60  
 QY 62 DRIEMKKIQDEQTYVFFDNKIQDLAGRAEILKTSKIMNVTFRDSALYRCEVVAR 121  
 DB 61 DRIEMKKIQDEQTYVFFDNKIQDLAGRAEILKTSKIMNVTFRDSALYRCEVVAR 120  
 QY 122 DRKEIDEIVIELTVQVKPTVPCRYPKAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 181  
 DB 122 DRKEIDEIVIELTVQVKPTVPCRYPKAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 180  
 QY 182 TDSRANPRFRNSSFHLNSETGLVFTAVHKDMSGQYCIASNDASARCEQEMEYDYL 241  
 DB 181 TDSRANPRFRNSSFHLNSETGLVFTAVHKDMSGQYCIASNDASARCEQEMEYDYL 240  
 QY 242 IGGIIGVLYLAVLALITLIGICAYRGRYFINNKQDESEYKPNKPGVNIYRTDEEG 301  
 DB 241 IGGIIGVLYLAVLALITLIGICAYRGRYFINNKQDESEYKPNKPGVNIYRTDEEG 300  
 QY 302 FRRHKSFEVI 310  
 DB 301 FRRHKSFEVI 309  
 RESULT 3  
 ID 09DB87 PRELIMINARY; PRT; 310 AA.  
 AC 09DB87  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE 1110002N23RIK PROTEIN.  
 GN JCMW2 OR 1110002N23RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=SMALL, INTESTINE;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito K.,  
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:39:08 : Search time 52.83 Seconds  
(without alignments)  
651.767 Million cell updates/sec

Title: US-09-524-531C-15

Perfect score: 310  
Sequence: 1 MALRRPRRLRCARLPDFLL.....VNYIRDESDGFRHKSSEFYI 310

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*  
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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                 |
|------------|-------|-------------|--------|-------|-----------------------------|
| 1          | 310   | 100.0       | 310    | 21    | AAB27276 Human confuency r  |
| 2          | 310   | 100.0       | 310    | 21    | AAB33457 Human PRO168 prot  |
| 3          | 310   | 100.0       | 310    | 21    | AAY36735 PRO168, an A33 an  |
| 4          | 310   | 100.0       | 310    | 22    | AAM93323 Human polypeptide, |
| 5          | 310   | 100.0       | 310    | 22    | AAM93905 Human polypeptide, |
| 6          | 310   | 100.0       | 310    | 22    | AAU12440 Human PRO168 poly  |
| 7          | 310   | 100.0       | 310    | 22    | AAB80272 Human PRO168 prot  |
| 8          | 310   | 100.0       | 310    | 22    | AAB80383 Secreted protein e |
| 9          | 310   | 100.0       | 310    | 22    | AAB80408 Secreted protein e |
| 10         | 310   | 100.0       | 310    | 22    | AAB80409 Secreted protein e |
| 11         | 310   | 100.0       | 311    | 21    | AAB38333 Human secreted pro |

|    |     |       |     |    |                             |
|----|-----|-------|-----|----|-----------------------------|
| 12 | 310 | 100.0 | 311 | 21 | AAB38383 Human secreted pro |
| 13 | 310 | 100.0 | 311 | 21 | AAB38384 Human secreted pro |
| 14 | 310 | 100.0 | 339 | 22 | AAB80431 Gene #13 associate |
| 15 | 209 | 67.4  | 310 | 21 | AAY36294 Human IGFAM-6 Immu |
| 16 | 161 | 51.9  | 285 | 21 | AAB39254 Human secreted pro |
| 17 | 151 | 48.7  | 291 | 22 | ABG04645 Novel human diagno |
| 18 | 151 | 48.7  | 404 | 22 | ABG12109 Novel human diagno |
| 19 | 104 | 33.5  | 361 | 22 | ABG22401 Novel human diagno |
| 20 | 89  | 28.7  | 89  | 20 | AA111472 Human 5' EST seque |
| 21 | 63  | 20.3  | 267 | 22 | ABG27038 Novel human diagno |
| 22 | 51  | 16.5  | 264 | 22 | ABG07157 Novel human diagno |
| 23 | 51  | 16.5  | 301 | 22 | ABG22399 Novel human diagno |
| 24 | 38  | 12.3  | 68  | 22 | ABG22398 Novel human diagno |
| 25 | 24  | 7.7   | 310 | 21 | AAB27272 Human confuency r  |
| 26 | 24  | 7.7   | 310 | 21 | AAB27276 Human confuency r  |
| 27 | 8   | 2.6   | 31  | 22 | ABB29193 Peptide #1844 enco |
| 28 | 8   | 2.6   | 31  | 22 | ABB34350 Peptide #1856 enco |
| 29 | 8   | 2.6   | 31  | 22 | ABB19769 Protein #1768 enco |
| 30 | 8   | 2.6   | 31  | 22 | AAM55147 Human brain expres |
| 31 | 8   | 2.6   | 31  | 22 | AAM67540 Human bone marrow  |
| 32 | 8   | 2.6   | 31  | 22 | AAM15353 Peptide #1787 enco |
| 33 | 8   | 2.6   | 31  | 22 | AAM27831 Peptide #1868 enco |
| 34 | 8   | 2.6   | 31  | 22 | AAM03112 Arabidopsis thalia |
| 35 | 8   | 2.6   | 120 | 21 | AAG30027 Arabidopsis thalia |
| 36 | 8   | 2.6   | 154 | 21 | AAG30026 Arabidopsis thalia |
| 37 | 8   | 2.6   | 190 | 21 | AAG30025 Arabidopsis thalia |
| 38 | 7   | 2.3   | 21  | 21 | AAB27269 Murine CRAW-1 tyro |
| 39 | 7   | 2.3   | 12  | 16 | AAR83341 Kb-binding Random  |
| 40 | 7   | 2.3   | 14  | 16 | AAR83451 Arabidopsis thalia |
| 41 | 7   | 2.3   | 39  | 22 | ABB31269 Human secreted pro |
| 42 | 7   | 2.3   | 39  | 22 | ABB31269 Peptide #3920 enco |
| 43 | 7   | 2.3   | 39  | 22 | ABB31269 Peptide #3983 enco |
| 44 | 7   | 2.3   | 39  | 22 | ABB21819 Protein #3818 enco |
| 45 | 7   | 2.3   | 39  | 22 | AAM59641 Human brain expres |
| 46 | 7   | 2.3   | 39  | 22 | AAM17457 Human bone marrow  |
| 47 | 7   | 2.3   | 39  | 22 | AAM29977 Peptide #4014 enco |
| 48 | 7   | 2.3   | 39  | 22 | AAM05154 Peptide #3816 enco |
| 49 | 7   | 2.3   | 40  | 22 | AAG74530 Human colon cancer |
| 50 | 7   | 2.3   | 56  | 22 | AA004488 Human polypeptide  |
| 51 | 7   | 2.3   | 58  | 22 | AA049383 Protonibacterium   |
| 52 | 7   | 2.3   | 67  | 21 | AAG34555 Arabidopsis thalia |
| 53 | 7   | 2.3   | 70  | 21 | AAG34554 Arabidopsis thalia |
| 54 | 7   | 2.3   | 71  | 22 | AA011264 Human polypeptide  |
| 55 | 7   | 2.3   | 73  | 22 | AAU39482 Protonibacterium   |
| 56 | 7   | 2.3   | 78  | 22 | ABG29189 Novel human diagno |
| 57 | 7   | 2.3   | 87  | 22 | AAU19792 Human novel extrac |
| 58 | 7   | 2.3   | 89  | 21 | AAG59037 Human secreted pro |
| 59 | 7   | 2.3   | 92  | 21 | AAG59054 Arabidopsis thalia |
| 60 | 7   | 2.3   | 92  | 21 | AAG60335 Arabidopsis thalia |
| 61 | 7   | 2.3   | 92  | 21 | AAV73830 Human prostate tum |
| 62 | 7   | 2.3   | 102 | 20 | AAV73830 Human prostate tum |
| 63 | 7   | 2.3   | 104 | 22 | AAO09976 Human polypeptide  |
| 64 | 7   | 2.3   | 106 | 22 | AAG82299 S. epidermidis ope |
| 65 | 7   | 2.3   | 110 | 21 | AAG59053 Arabidopsis thalia |
| 66 | 7   | 2.3   | 110 | 21 | ABG04070 Novel human diagno |
| 67 | 7   | 2.3   | 127 | 22 | AAV38779 Human secreted pro |
| 68 | 7   | 2.3   | 149 | 20 | AAV38779 Neisseria meningit |
| 69 | 7   | 2.3   | 152 | 21 | AAG58379 Arabidopsis thalia |
| 70 | 7   | 2.3   | 158 | 21 | AAG60639 Arabidopsis thalia |
| 71 | 7   | 2.3   | 162 | 18 | AAW20313 H. pylori surface  |
| 72 | 7   | 2.3   | 172 | 21 | AAG16559 Arabidopsis thalia |
| 73 | 7   | 2.3   | 173 | 21 | AAG58378 Arabidopsis thalia |
| 74 | 7   | 2.3   | 173 | 21 | Arabidopsis thalia          |
| 75 | 7   | 2.3   | 175 | 21 | Arabidopsis thalia          |

#### ALIGNMENTS

RESULT 1  
AAB27276 standard; Protein: 310 AA.  
ID AAB27276 standard; Protein: 310 AA.  
xx

| Query Match           | 100.0%  | Score 310          | DB 21    | Length 310 |
|-----------------------|---|--------------------|----------|------------|
| Best Local Similarity | 100.0%  | Pred. No. 1.7e-295 |          |            |
| Matches 310           | Conservative 0  | Mismatches 0       | Indels 0 | Gaps 0     |
| 1                     | MALRRPRLRLCARLDELFFLLLFRCGLIGAVNLKSSNRPVVOEFESVELSCITRDSOT  | 60                 |          |            |
| 1                     | MAIRRPRLRLCARLDELFFLLLFRCGLIGAVNLKSSNRPVVOEFESVELSCITRDSOT  | 60                 |          |            |
| 61                    | SDPRIMWKRIODEQTYYVEFDNKIGDGLAGRAELIGKTSIKIMNTRDSALYRCVVAR   | 120                |          |            |
| 61                    | SDPRIMWKRIODEQTYYVEFDNKIGDGLAGRAELIGKTSIKIMNTRDSALYRCVVAR   | 120                |          |            |
| 121                   | NDEKELDEIVIELTVOVKPPTVCGRPKAVPVGKMTLLCOSEEGHPRPHYSMYRNDVPL  | 180                |          |            |
| 121                   | NDEKELDEIVIELTVOVKPPTVCGRPKAVPVGKMTLLCOSEEGHPRPHYSMYRNDVPL  | 180                |          |            |
| 181                   | PTDSRANPRFRNSSFHLNSETGTLVETAHKDSDGQYCIASNDAGSARCEQEMEVYDL   | 240                |          |            |
| 181                   | PTDSRANPRFRNSSFHLNSETGTLVETAHKDSDGQYCIASNDAGSARCEQEMEVYDL   | 240                |          |            |
| 241                   | NIGGITGGVLYVLAVALITLIGICCAIRRGYIFNNKQDESGYNNPKRPGVNTIRIDEGS | 300                |          |            |
| 241                   | NIGGITGGVLYVLAVALITLIGICCAIRRGYIFNNKQDESGYNNPKRPGVNTIRIDEGS | 300                |          |            |
| 301                   | DFRHKSSFYI 310  |                    |          |            |
| 301                   | DFRHKSSFYI 310  |                    |          |            |

|          |  |
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| AAB33457 | standard; Protein: 310 AA.   |
| AC       | AAB33457;  |
| XX       |  |
| DT       | 29-JAN-2001 (first entry)  |
| XX       |  |
| DE       | Human PRO1868 protein UNQ059 SEQ ID NO:193.                            |
| XX       |  |
| KM       | Human; immune related disease; diagnosis; antiinflammatory; cardiant;  |
| KM       | dermatologic; antrialthritic; antithematic; immunosuppressive;         |
| KM       | haemostatic; antithyroid; antidiabetic; neutropic; neuroprotective;    |
| KM       | antiaiemic; hepatotropic; vitruide; antiporiatic; antiallergic;        |
| KM       | antiaismatic; systemic lupus erythematosus; rheumatoid arthritis;      |
| KM       | osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  |
| KM       | idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;     |
| KM       | systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; |
| KM       | autoimmune thrombocytopenia; immune-mediated renal disease;            |
| KM       | demyelinating disease; hepatobiliary disease; Whipple's disease;       |
| KM       | inflammatory bowel disease; gluten-sensitive enteropathy;              |
| KM       | autoimmune disease; immune-mediated skin disease; allergic disease;    |
| KM       | immunological disease; transplantation associated disease;             |
| KM       | graft rejection; graft-versus-host-disease.                            |
| XX       |  |
| OS       | Homo sapiens.  |
| XX       |  |
| PN       | WO20003758-A2.   |
| XX       |  |
| PD       | 14-SEP-2000.   |
| XX       |  |
| PF       | 02-MAR-2000; 2000WO-US05841.   |
| XX       |  |
| PR       | 08-MAR-1999; 99WO-US05028.   |
| PR       | 10-MAR-1999; 99US-0123618.   |
| PR       | 12-MAR-1999; 99US-0123957.   |
| PR       | 23-MAR-1999; 99US-0125779.   |
| PR       | 12-APR-1999; 99US-0128849.   |
| PR       | 20-APR-1999; 99WO-US08615.   |
| PR       | 28-APR-1999; 99US-0131445.   |
| PR       | 04-MAY-1999; 99US-0132371.   |
| PR       | 14-MAY-1999; 99US-0134287.   |
| PR       | 02-JUN-1999; 99WO-US12252.   |
| PR       | 23-JUN-1999; 99US-0141037.   |
| PR       | 20-JUL-1999; 99US-0144756.   |
| PR       | 26-JUL-1999; 99US-0145696.   |
| PR       | 28-JUL-1999; 99US-0146222.   |
| PR       | 01-SEP-1999; 99WO-US20111.   |
| PR       | 08-SEP-1999; 99WO-US20594.   |
| PR       | 13-SEP-1999; 99WO-US20944.   |
| PR       | 15-SEP-1999; 99WO-US21090.   |
| PR       | 05-SEP-1999; 99WO-US21547.   |
| PR       | 05-OCT-1999; 99WO-US22089.   |
| PR       | 29-OCT-1999; 99US-0162506.   |
| PR       | 29-NOV-1999; 99WO-US28214.   |
| PR       | 30-NOV-1999; 99WO-US28313.   |
| PR       | 30-NOV-1999; 99WO-US28409.   |
| PR       | 01-DEC-1999; 99WO-US28301.   |
| PR       | 01-DEC-1999; 99WO-US28634.   |
| PR       | 02-DEC-1999; 99WO-US28551.   |
| PR       | 02-DEC-1999; 99WO-US28564.   |
| PR       | 02-DEC-1999; 99WO-US28565.   |
| PR       | 16-DEC-1999; 99WO-US30099.   |
| PR       | 20-DEC-1999; 99WO-US30999.   |
| PR       | 30-DEC-1999; 99WO-US31274.   |
| PR       | 05-JAN-2000; 2000WO-US00219.   |
| PR       | 06-JAN-2000; 2000WO-US00277.   |
| PR       | 06-JAN-2000; 2000WO-US00376.   |
| PR       | 11-FEB-2000; 2000WO-US03565.   |
| PR       | 18-FEB-2000; 2000WO-US04341.   |
| PR       | 18-FEB-2000; 2000WO-US04342.   |
| PR       | 22-FEB-2000; 2000WO-US04414.   |
| XX       |  |
| PA       | (GETH ) GENENTECH INC.   |

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 DR WPI: 2000-572271/53.  
 N-PSDB: AAC58622.

PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 PS Claim 33: Fig 88: 309pp: English.

CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 310 AA:

Query Match 100.0%; Score 310; DB 21; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-295;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 malrrprrlrcarlpdffllfrgcllgavnlksnrtprvqefesvlsclitdsqt 60  
 OY 61 SPPRIEMKKIOBQTYTVFEDNKIOGDLGRAEIIKSTSLKTNWTRRSALRYCVAR 120  
 DB 61 sppriewkkidqetlyvfndkligdlaigraeilgktslktnwtrrsalrycvar 120  
 OY 121 NDRKEIDEIVIELTVQKRPVPCRVKAVPVGKMATLHCQSESGHPRPHYSMYRNDVPL 180  
 DB 121 ndrkeideivieltvqkrpvpcrvkavpvgkmatlhcsesghprphysmyrndvpl 180  
 OY 181 PIDSRRANPRFRNSFHLNSETGTLVFTAVHKDSCGYCIASNDAGSARCEQEMEVYDL 240  
 DB 181 pidsrranprfrnsfhlsetgtlvftavhkddsgyyciasndagsarceeqemevydl 240  
 OY 241 NIGGIIGVLYVIALTLTGICCAVRGRGYFLNKKODESKRNPKKPGVWYIRRDGEG 300  
 DB 241 niggiigvlyvialtltgiccavrgrgyflnkkodeSKRNPKKPGVWYIRRDGEG 300  
 OY 301 DFRHKSFEVI 310  
 DB 301 dfrhksfevl 310

RESULT 3  
 ID AAY96735  
 XX AAY96735 standard; Protein: 310 AA.  
 AC AAY96735;  
 XX  
 DT 26-SEP-2000 (first entry)

XX DE PRO1868, an A33 antigen homologue.  
 XX KW PRO1868; A33 antigen; secreted protein; transmembrane protein;  
 KW anti-inflammatory; cytostatic; recombinant production; gene therapy.  
 OS Homo sapiens.

| Key           | Location/Qualifiers   |
|---------------|---|
| Peptide       | 1..30   |
| Modified-site | /label= Signal_peptide  |
| Modified-site | 26..31  |
| Modified-site | /note= "N-myristoylation site"  |
| Modified-site | 69..77  |
| Modified-site | /note= "Tyrosine kinase phosphorylation site"                         |
| Modified-site | 104..107  |
| Modified-site | /note= "N-glycosylation site"   |
| Modified-site | 106..109  |
| Modified-site | /note= "Casein kinase II phosphorylation site"                        |
| Modified-site | 107..110  |
| Modified-site | /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site" |
| Modified-site | 192..195  |
| Modified-site | /note= "N-glycosylation site"   |
| Modified-site | 215..220  |
| Modified-site | /note= "N-myristoylation site"  |
| Modified-site | 226..231  |
| Modified-site | /note= "N-myristoylation site"  |
| Domain        | 243..263  |
| Modified-site | /label= Transmembrane_domain  |
| Modified-site | 243..248  |
| Modified-site | /note= "N-myristoylation site"  |
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| Modified-site | /note= "N-myristoylation site"  |
| Modified-site | 262..267  |
| Modified-site | /note= "N-myristoylation site"  |
| Modified-site | 296..299  |
| Modified-site | /note= "Casein kinase II phosphorylation site"                        |

WO200036102-A2.  
 22-JUN-2000.  
 01-DEC-1999; 99WO-US28634.  
 16-DEC-1998; 98US-0112851.  
 16-DEC-1998; 98US-0113145.  
 22-DEC-1998; 98US-0113511.  
 12-JAN-1999; 99US-0115558.  
 12-JAN-1999; 99US-0115565.  
 12-JAN-1999; 99US-0115733.  
 09-FEB-1999; 99US-0119341.  
 10-FEB-1999; 99US-0119537.  
 12-FEB-1999; 99US-0119965.  
 02-JUN-1999; 99WO-US12252.

(GETH ) GENENTECH INC.  
 PA  
 XX Bozstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;  
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX  
 DR WPI: 2000-431586/37.  
 DR N-PSDB: AAA51265.

Isolated nucleic acid molecule encodes a PRO polypeptide which is a  
 transmembrane polypeptide  
 Claim 1; Fig 14; 154pp: English.

This is PRO1868, a putative homologue of A33 antigen, a known  
 colorectal cancer-associated marker. The invention concerns novel  
 secreted and transmembrane proteins, designated PRO polypeptides. The





PA3' (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX  
 DR WPI: 2001-524255/58.  
 DR N-PSDB: AAK94867.  
 XX  
 PT 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -  
 XX  
 PS Claim 8: SEQ ID NO 4051; 1380bp + sequence listing; English.  
 CC  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
 CC molecules have been determined. Primers for synthesizing the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a polypeptide  
 CC encoded by a full length human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 CC  
 XX  
 SO Sequence 310 AA:

Query Match 100.0%; Score 310; DB 22; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-295;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAIRRRPRLRLCARLPDFLLIFRGCLTGAVALKSNRPVQEFSEVSLCITDSOT 60  
 DB 1 MAIRRRPRLRLCARLPDFLLIFRGCLTGAVALKSNRPVQEFSEVSLCITDSOT 60  
 OY 61 SDPRLEMKRIODEQTYVFEFNKIQODLAGRAEILKTSIKINWVRSDALRCEVVAR 120  
 DB 61 SDPRLEMKRIODEQTYVFEFNKIQODLAGRAEILKTSIKINWVRSDALRCEVVAR 120  
 OY 121 NDRKEIDEIVIELTVQVKPVPCRVKAVPVGKMATLHCQEGSHPRPHYSVRNDVPL 180  
 DB 121 NDRKEIDEIVIELTVQVKPVPCRVKAVPVGKMATLHCQEGSHPRPHYSVRNDVPL 180  
 OY 181 PDSRANPPRRNSFFLNSTGLVFTVAHKDSCGYCTCLASNDASAREEDBEMEYDL 240  
 DB 181 PDSRANPPRRNSFFLNSTGLVFTVAHKDSCGYCTCLASNDASAREEDBEMEYDL 240  
 OY 241 NIGGIGVLYVALALITLGICAVRRGYFINNKODGSEYKPKGPDGVNIRTDDEG 300  
 DB 241 NIGGIGVLYVALALITLGICAVRRGYFINNKODGSEYKPKGPDGVNIRTDDEG 300  
 OY 301 DFRHNSFWI 310  
 DB 301 DFRHNSFWI 310  
 OY 301 dfthksfvl 310  
 DB 301 dfthksfvl 310

RESULT 6  
 AAU12440  
 ID AAU12440 standard; Protein: 310 AA.  
 XX  
 AC AAU12440;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human PRO1868 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.  
 XX

OS Homo sapiens.  
 XX  
 PN MO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000MO-US32678.  
 XX  
 PR 01-DEC-1999; 99MO-US28301.  
 PR 01-DEC-1999; 99MO-US28634.  
 PR 02-DEC-1999; 99MO-US28551.  
 PR 02-DEC-1999; 99MO-US28564.  
 PR 02-DEC-1999; 99MO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 30-DEC-1999; 99MO-US30999.  
 PR 06-JAN-2000; 2000MO-US03277.  
 PR 06-JAN-2000; 2000MO-US00376.  
 PR 11-FEB-2000; 2000MO-US03565.  
 PR 18-FEB-2000; 2000MO-US04341.  
 PR 18-FEB-2000; 2000MO-US04342.  
 PR 22-FEB-2000; 2000MO-US04414.  
 PR 24-FEB-2000; 2000MO-US04914.  
 PR 24-FEB-2000; 2000MO-US05004.  
 PR 01-MAR-2000; 2000MO-US05601.  
 PR 20-MAR-2000; 2000MO-US07377.  
 PR 21-MAR-2000; 2000MO-US07532.  
 PR 30-MAR-2000; 2000MO-US08439.  
 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14941.  
 PR 02-JUN-2000; 2000MO-US15264.  
 PR 10-NOV-2000; 2000MO-US30873.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Geritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;  
 XX  
 DR WPI: 2001-408281/43.  
 DR N-PSDB: AAS21512.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 XX  
 PS Claim 12: Fig 538: 813bp; English.  
 PS  
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 XX

SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 22; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-295;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRCARLPDFFLLFRGCLIGAVNLKSSNRTPVVOEFSEVLSCLITDSQT 60  
 Db 1 malrrprrlrcarlpdflllfrgcllgavnlkssnrtpvvgesfvelsciltdsq 60  
 QY 61 SDRPIEMKKIQDEQTYVFFDNKIQGLAGRAELIGKTSKIMWVTRDSALYCEVVAR 120  
 Db 61 sdprlwmkklqdeqtlvffdnkigqlagraeligktslkimvtrdsalycvvar 120  
 QY 121 NDRKEIDEIVIELTVQKVPVPCRVKPAVPGKMATLHCQESGHPRHPSWYRNDVPL 180  
 Db 121 ndrkeideivieltvqkvpvpcrvpkavpgkmatlhcgeseqhprphyswyrndvpl 180  
 Db 181 PTDSRANPRFRNSSFHLNSETGTVFPAVHKDSDGQYYCIASNDAGSARCEQDEMEYVDL 240  
 Db 181 ptdsrnprfrnssfhlntsetgtlvfpavhkdsdgqyyciasndagsarceqdeyemeydl 240  
 QY 241 NIGGIIIGVVLAVLALITGICCAVRGYFINNKODGESYKMPKPGDGVNYIRTDSEG 300  
 Db 241 niggiigvvlavlaalitgiccayrgrgyfnnkqdgesyknpgpdyvnyirtdseg 300  
 QY 301 DFRHKSSEFVI 310  
 Db 301 dfrhkssefvi 310

## RESULT 7

AAAB0272  
 ID AAB0272 standard; protein: 310 AA.

AC AAB0272;

XX 24-APR-2001 (first entry)

XX Human PRO1868 protein.

XX Human: PRO: dermatological; antipruritic; cytoprotective; antiinflammatory;  
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiact;  
 KW antiangiogenic; vasotrophic; antiautomatic; antineumatic; cancer;  
 KW antiarthritic; antiferility; antidiabetic; antiviral; diabetes;  
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;  
 ischaemia; inflammation.

XX Homo sapiens.

XX WO200104311-A1.

XX 18-JAN-2001.

XX 22-FEB-2000; 2000WO-US04414.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 05-JAN-2000; 99WO-US00219.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N,  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,  
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ,  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,  
 PI Williams PM, Wood WI;  
 XX WPI: 2001-081051/09.  
 DR N-PSDB: AAF72433.

PT Sixty one nucleic acids encoding PRO polypeptides which are useful in  
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung  
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.  
 PT Alzheimer's disease) -

XX Claim 1; Fig 124; 393pp; English.

CC The present sequence is one of sixty one novel secreted and  
 CC transmembrane PRO polypeptides. The PRO polypeptides are  
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.  
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,  
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.  
 CC endometrial bleeding, angiogenesis, ischaemia) such as coronary  
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,  
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and  
 CC diabetes and retinal disorders such as retinitis pigmentosa.  
 CC The PRO nucleic acids have applications in molecular biology, including  
 CC use as hybridization probes, and in chromosome and gene mapping.

XX Sequence 310 AA;

Query Match 100.0%; Score 310; DB 22; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-295;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRCARLPDFFLLFRGCLIGAVNLKSSNRTPVVOEFSEVLSCLITDSQT 60  
 Db 1 malrrprrlrcarlpdflllfrgcllgavnlkssnrtpvvgesfvelsciltdsq 60  
 QY 61 SDRPIEMKKIQDEQTYVFFDNKIQGLAGRAELIGKTSKIMWVTRDSALYCEVVAR 120  
 Db 61 sdprlwmkklqdeqtlvffdnkigqlagraeligktslkimvtrdsalycvvar 120  
 QY 121 NDRKEIDEIVIELTVQKVPVPCRVKPAVPGKMATLHCQESGHPRHPSWYRNDVPL 180  
 Db 121 ndrkeideivieltvqkvpvpcrvpkavpgkmatlhcgeseqhprphyswyrndvpl 180  
 QY 181 PTDSRANPRFRNSSFHLNSETGTVFPAVHKDSDGQYYCIASNDAGSARCEQDEMEYVDL 240  
 Db 181 ptdsrnprfrnssfhlntsetgtlvfpavhkdsdgqyyciasndagsarceqdeyemeydl 240  
 QY 241 NIGGIIIGVVLAVLALITGICCAVRGYFINNKODGESYKMPKPGDGVNYIRTDSEG 300  
 Db 241 niggiigvvlavlaalitgiccayrgrgyfnnkqdgesyknpgpdyvnyirtdseg 300  
 QY 301 DFRHKSSEFVI 310  
 Db 301 dfrhkssefvi 310

## RESULT 8

AAAB0383  
 ID AAB0383 standard; protein: 310 AA.

XX AAB0383;

XX 24-APR-2001 (first entry)

XX Secreted protein encoded by gene #13.

XX Secreted protein; human; autoimmune; hyperproliferation;

KW 5' cardiovascular; cerebrovascular; infection; food.  
XX  
XX OS Homo sapiens.  
XX  
XX MN WO200107459-A1.  
XX  
XX PD 01-FEB-2001.  
XX  
XX PE 20-JUL-2000; 2000WO-US19735.  
XX  
XX PR 23-JUL-1999; 99US-0145220.  
XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;  
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;  
XX  
XX DR WPI; 2001-123261/13.  
XX  
XX PT New isolated nucleic acid encoding 29 secreted proteins, for  
XX diagnosing, preventing and treating e.g. autoimmune,  
XX hyperproliferative, cardiovascular, and ocular diseases or disorders  
XX and microorganism infections  
XX  
XX PS Claim 11: Page 538-539; 601pp; English.  
XX  
XX CC The present invention relates to 29 human secreted proteins. The  
XX invention is used to prevent autoimmune diseases e.g. rheumatoid  
XX arthritis, hyperproliferative disorders e.g. neoplasms of the  
XX breast or liver, cardiovascular disorders e.g. cardiac arrest,  
XX cerebrovascular disorders e.g. cerebral ischemia, angiodenesis,  
XX nervous system disorders e.g. Alzheimer's disease, infections  
XX caused by bacteria, viruses and fungi and ocular disorders e.g.  
XX corneal infection. Also used in food preparations.  
XX  
XX SQ Sequence 310 AA;  
  
Query Match 100.0%; Score 310; DB 22; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.7e-295;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQVEFESVELSCIITDSOT 60  
DB 1 malrrprrlrlcarlpdfflllfrgcllgavnlksnrtpvqgefesvelscitdsqt 60  
QY 61 SDPRIEMKKIODEQTTVFFDNKIOGDLAGRAEILGKTSLKIMWTRRDSALYRCEVVAR 120  
DB 61 sdpriemkkiodeqttvffdnkiogdlagraeilgktslkimwtrrdsalyrcevar 120  
QY 121 NDRKEIDIVIELTQVQVPVPCVPRKAVPVGKMATLHCQESGHPHYSMYRNDVPL 180  
DB 121 ndrkeideivleltqvvpvpcvprkavpvgkmatlhqeseghprphysmyrndvpl 180  
QY 181 PTDSRANRFRNSSFHLSSETGLVFTAVHKDDSGOYCIASNDAGSARCEQEMEYVDL 240  
DB 181 ptdsranrfrnssfhlsssetglvftavhkddsgoyciandsagarsceqemevydl 240  
QY 241 NIGGIIGVLYVAVLALITGICACAYRGRGFYINNKODESEYKNGKPDGVNYIRTDEEG 300  
DB 241 niggiigvlyvavlalitgicacayrgrgyfinnkodeseykngkpdgvnyirtdeeg 300  
QY 301 DFRHSSFVI 310  
DB 301 dfrhssfvf 310  
  
RESULT 9  
AAB80408  
ID AAB80408 standard; protein: 310 AA.  
XX  
XX AAB80408;  
XX

DT 24-APR-2001 (first entry)  
XX  
XX DE Secreted protein encoded by gene #38.  
XX  
XX KW Secreted protein; human; autoimmune; hyperproliferation;  
XX cardiovascular; cerebrovascular; infection; food.  
XX  
XX OS Homo sapiens.  
XX  
XX MN WO200107459-A1.  
XX  
XX PD 01-FEB-2001.  
XX  
XX PE 20-JUL-2000; 2000WO-US19735.  
XX  
XX PR 23-JUL-1999; 99US-0145220.  
XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;  
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;  
XX  
XX DR WPI; 2001-123261/13.  
XX  
XX PT New isolated nucleic acid encoding 29 secreted proteins, for  
XX diagnosing, preventing and treating e.g. autoimmune,  
XX hyperproliferative, cardiovascular, and ocular diseases or disorders  
XX and microorganism infections  
XX  
XX PS Claim 11: Page 557-558; 601pp; English.  
XX  
XX CC The present invention relates to 29 human secreted proteins. The  
XX invention is used to prevent autoimmune diseases e.g. rheumatoid  
XX arthritis, hyperproliferative disorders e.g. neoplasms of the  
XX breast or liver, cardiovascular disorders e.g. cardiac arrest,  
XX cerebrovascular disorders e.g. cerebral ischemia, angiodenesis,  
XX nervous system disorders e.g. Alzheimer's disease, infections  
XX caused by bacteria, viruses and fungi and ocular disorders e.g.  
XX corneal infection. Also used in food preparations.  
XX  
XX SQ Sequence 310 AA;  
  
Query Match 100.0%; Score 310; DB 22; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.7e-295;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQVEFESVELSCIITDSOT 60  
DB 1 malrrprrlrlcarlpdfflllfrgcllgavnlksnrtpvqgefesvelscitdsqt 60  
QY 61 SDPRIEMKKIODEQTTVFFDNKIOGDLAGRAEILGKTSLKIMWTRRDSALYRCEVVAR 120  
DB 61 sdpriemkkiodeqttvffdnkiogdlagraeilgktslkimwtrrdsalyrcevar 120  
QY 121 NDRKEIDIVIELTQVQVPVPCVPRKAVPVGKMATLHCQESGHPHYSMYRNDVPL 180  
DB 121 ndrkeideivleltqvvpvpcvprkavpvgkmatlhqeseghprphysmyrndvpl 180  
QY 181 PTDSRANRFRNSSFHLSSETGLVFTAVHKDDSGOYCIASNDAGSARCEQEMEYVDL 240  
DB 181 ptdsranrfrnssfhlsssetglvftavhkddsgoyciandsagarsceqemevydl 240  
QY 241 NIGGIIGVLYVAVLALITGICACAYRGRGFYINNKODESEYKNGKPDGVNYIRTDEEG 300  
DB 241 niggiigvlyvavlalitgicacayrgrgyfinnkodeseykngkpdgvnyirtdeeg 300  
QY 301 DFRHSSFVI 310  
DB 301 dfrhssfvf 310  
  
RESULT 10

AAB80409  
ID AAB80409 standard; protein; 310 AA.  
XX  
AC AAB80409;  
XX  
DT 24-APR-2001 (first entry)  
XX  
DE Secreted protein encoded by gene #39.  
XX  
KW Secreted protein; human; autoimmune; hyperproliferation;  
KW cardiovascular; cerebrovascular; infection; food.  
XX  
OS Homo sapiens.  
PN MO200107459-A1.  
XX  
PD 01-FEB-2001.  
XX  
PR 20-JUL-2000; 2000MO-US19735.  
XX  
23-JUL-1999; 99US-0145220.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;  
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;  
XX WPI: 2001-123261/13.  
XX  
PT New isolated nucleic acid encoding 29 secreted proteins, for  
PT diagnosing, preventing and treating e.g. autoimmune,  
PT hyperproliferative, cardiovascular, and ocular diseases or disorders  
PT and microorganism infections  
XX  
PS Claim 11: Page 559-560; 601pp; English.  
XX  
CC The present invention relates to 29 human secreted proteins. The  
CC invention is used to prevent autoimmune diseases e.g. rheumatoid  
CC arthritis, hyperproliferative disorders e.g. neoplasms of the  
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,  
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,  
CC nervous system disorders e.g. Alzheimer's disease, infections  
CC caused by bacteria, viruses and fungi and ocular disorders e.g.  
CC corneal infection. Also used in food preparations.  
XX  
SQ Sequence 310 AA:  
XX  
Query Match 100.0%; Score 310; DB 22; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.7e-295;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 MAIRPRRLRLCARLPDFLLFRGLIGAVNLKSNRTPVVOEFSEVSLCITTSQT 60  
DB 1 mairprlrlcarlpdfflllfrgcligaavnlkssnrtpvvqefesvelscitltsqt 60  
QY 61 SDBRIEMKKIODEQTYVFPDNKIQDLAGRAELIGTSKIMVWTRRDSALYCEVVAR 120  
DB 61 sdbrleemkkiodeqtyvfpdnkiqdglaagraellgtsklmvttrdsalyccevar 120  
QY 121 NDKREIDELIETLVQKPTPCRVKAVPVGKMATLHCQESGHRPHYSWRNDVPL 180  
DB 121 ndkreidelietlvqkptpcrvkavpvvgkmatlhqeseghrphyswyrndvpl 180  
QY 121 PTDSPANRPRNSSEFHNSETGLVFAVHKDGGYYCIASNDAGSARCEOEEMEYDL 240  
DB 181 ptdspanrprnssefhnsetglvfaavhkddsggyyciasndagsarceegemeeydl 240  
QY 241 NIGGIIGVAVLAVLALITLGICAYRRGYFINNKODGESYKNGKPGPDGVNVRTDEG 300  
DB 241 niggiigvavlvallitlgicayrrgyfinnkodgesyknpgpdgvnvyrtdeeg 300  
QY 301 DFRHKSSEFV 310

DB 301 dfrhkssefvl 310  
XXXXXXXXXX  
RESULT 11  
ID AAB38333 standard; Protein; 311 AA.  
XX  
AC AAB38333;  
XX  
DT 31-JAN-2001 (first entry)  
XX  
DE Human secreted protein encoded by gene 13 clone HAPSA79.  
XX  
KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;  
KW cytostatic; cardiact; vasotropic; cerebroprotective; neuroprotective;  
KW nootropic; antibacterial; virucide; fungicide; optalmalological; human;  
KW vulnerary; gene therapy; infection; secreted protein.  
XX  
OS Homo sapiens.  
PN MO200061623-A1.  
XX  
PD 19-OCT-2000.  
XX  
PR 06-APR-2000; 2000MO-US08979.  
XX  
PR 09-APR-1999; 99US-0128693.  
XX 26-APR-1999; 99US-0130991.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PI Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;  
PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;  
XX Young PE;  
XX  
DR WPI: 2000-647418/62.  
XX  
PT New nucleic acid molecules encoding 62 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
PT used as food additives or preservatives  
XX  
XX  
PS Claim 11: Page 603-604; 716pp; English.  
XX  
CC Sequences AAB38321-B38396 represent the amino acid sequences of 62  
CC human secreted proteins encoded by the genes AAG69512-C69587. The genes  
CC and proteins are useful for preventing, ameliorating or treating medical  
CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
CC a range of human tissues disclosed in the specification. The nucleic  
CC acids, proteins, antibodies and (ant)agonists are useful in the  
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac  
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)  
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)  
CC infections caused by bacteria, viruses and fungi; and (h) ocular  
CC disorders e.g. corneal infection. The polypeptides can also be used to  
CC aid wound healing and epithelial cell proliferation, to prevent skin  
CC aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis.  
XX  
SQ Sequence 311 AA:  
XX  
Query Match 100.0%; Score 310; DB 21; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.7e-295;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 MAIRPRRLRLCARLPDFLLFRGLIGAVNLKSNRTPVVOEFSEVSLCITTSQT 60  
DB 1 mairprlrlcarlpdfflllfrgcligaavnlkssnrtpvvqefesvelscitltsqt 60

YY 61 SDPRLEWKKIODECQTYTFEPDNKIOGDLAGRAELIGKTSLKNNVTRRSDALYRCVEVAR 120  
Db 61 sdprlewwkIQdeqTlyfFdnkiqgdlaagraeligktslknnvtrrrsdalyrcevar 120  
QY 121 NDREIDIVIELTVQVPVTPVCVRPKAVGVGMKATLHCQESBGRPHYSWRNDVPL 180  
Db 121 ndrEIdElvIElTvqvkpvtpvcvrpkavpgvmAtlhcgEsBgRphyswRNdVpl 180  
QY 181 PTDSNANRFNFSSFFHLNSETGLVTFAVHKDSDSGOYYYCIASNDAGSARCEDEMEVYDL 240  
Db 181 ptdsnanrfnfnssffhlNsetglvtfaVhkdsdsgoYyyciAsndagsarceEdemeVydl 240  
QY 241 NIGGIIGVLVLAVALITIGTCARRGFITNNKDDSESKYPKGRPDGVNVRTDBEG 300  
Db 241 nIgGiIGvLVLaValItIGtCaRRgFItnNKddSeSkypKgRpDgvnVrtDbeg 300  
QY 301 DFRHKSFEVI 310  
Db 301 dfrhksfevi 310

JUL7 12  
AAB38383

ID AAB38383 standard; Protein: 311 AA.

AC AAB38383;  
XX  
DT 31-JAN-2001 (first entry)  
XX  
DE Human secreted protein encoded by gene 13 clone HAPS479.  
KM Immunosuppressive; antarthritic; antiheumatic; antiproliferative;  
KW cytosolic; cardiac; vasotropic; cerebroprotective; neuroprotective;  
KM neotrophic; antibacterial; virucide; fungicide; ophthalmological; human;  
XX vulnery; gene therapy; infection; secreted protein.  
XX Homo sapiens.  
OS  
XX  
PN WC200061623-A1.  
PD 19-OCT-2000.  
XX  
PF 06-APR-2000; 2000MO-US08979.  
XX  
PR 09-APR-1999; 99US-0128693.  
PR 26-APR-1999; 99US-0130991.  
XX (HUMA-) HUMAN GENOME SCI INC.

Ruben SM, NI J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;  
Lafleur DM, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;  
Young PE;  
WP1: 2000-647418/62.

New nucleic acid molecules encoding 62 human secreted proteins for  
diagnosing, preventing, treating or ameliorating medical conditions and  
used as food additives or preservatives -  
  
Claim 11: Page 642-643: 716pp: English.

PS Sequences AAB38321-B38396 represent the amino acid sequences of 62  
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes  
CC and proteins are useful for preventing, ameliorating or treating medical  
CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
CC a range of human tissues disclosed in the specification. The nucleic  
CC acids, proteins, antibodies and (ant)agonists are useful in the  
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
CC of the breast or liver; (c) cardiovascular disorders e.g. cerebral  
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)  
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)  
CC angiogenesis caused by bacteria, viruses and fungi; and (h) ocular

|           | Query Match  | 100.0%;         | Score 310;          | DB 21;    | Length 311; |
|-----------|--|-----------------|---------------------|-----------|-------------|
|           | Best Local Similarity  | 100.0%;         | Pred. No. 1.7e-295; |           |             |
|           | Matches 310;   | Conservative 0; | Mismatches 0;       | Indels 0; | Gaps 0      |
| CC        | disorders e.g. corneal infection. The polypeptides can also be used to   |                 |                     |           |             |
| CC        | aid wound healing and epithelial cell proliferation, to prevent skin     |                 |                     |           |             |
| CC        | aging due to sunburn, to maintain organs before transplantation, for     |                 |                     |           |             |
| CC        | supporting cell culture of primary tissues, to regenerate tissues and in |                 |                     |           |             |
| CC        | chemotaxis.  |                 |                     |           |             |
| xx        |  |                 |                     |           |             |
| SQ        | Sequence 311 AA:   |                 |                     |           |             |
| QY        | 1 MALRRPRRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRPVQGEFSEVELSCIITDSQT 60          |                 |                     |           |             |
| DB        | 1 MALRRPRRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRPVQGEFSEVELSCIITDSQT 60          |                 |                     |           |             |
| QY        | 61 SPPRIEMKKIODEQRTTYVFDMKIGQDLGAGRAEILCKTSLKTIWYTRRDSALYRCVVAR 120      |                 |                     |           |             |
| DB        | 61 SPPRIEMKKIODEQRTTYVFDMKIGQDLGAGRAEILCKTSLKTIWYTRRDSALYRCVVAR 120      |                 |                     |           |             |
| QY        | 121 NDRKEIDELVIELTVQVKRPVPCRVPRKAVPVGKMAATLQSESEGHPRPHYSWRNDVPL 180      |                 |                     |           |             |
| DB        | 121 NDRKEIDELVIELTVQVKRPVPCRVPRKAVPVGKMAATLQSESEGHPRPHYSWRNDVPL 180      |                 |                     |           |             |
| QY        | 181 PTDSRANPRFRNSSFHLNSETGTLVFTAVAHKDDSGQYCIASNDAGSARCEQEMEVYDL 240      |                 |                     |           |             |
| DB        | 181 PTDSRANPRFRNSSFHLNSETGTLVFTAVAHKDDSGQYCIASNDAGSARCEQEMEVYDL 240      |                 |                     |           |             |
| QY        | 241 NIGGIIIGVYLVAVLALTTLGICCAVRRNGYFIANKQDESKNPKRPGCVNTRIRDEG 300        |                 |                     |           |             |
| DB        | 241 NIGGIIIGVYLVAVLALTTLGICCAVRRNGYFIANKQDESKNPKRPGCVNTRIRDEG 300        |                 |                     |           |             |
| QY        | 301 DFRHKSSEFVI 310  |                 |                     |           |             |
| DB        | 301 DFRHKSSEFVI 310  |                 |                     |           |             |
| RESULT 13 |  |                 |                     |           |             |
| AAB38384  |  |                 |                     |           |             |
| ID        | AAB38384 standard; Protein: 311 AA.                                      |                 |                     |           |             |
| XX        | AAB38384:  |                 |                     |           |             |
| AC        | 31-JAN-2001 (first entry)  |                 |                     |           |             |
| DT        |  |                 |                     |           |             |
| XX        |  |                 |                     |           |             |
| DE        | Human secreted protein encoded by gene 13 clone HAPSAT79.                |                 |                     |           |             |
| XX        |  |                 |                     |           |             |
| KW        | Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;      |                 |                     |           |             |
| KW        | cytostatic; cardiatic; vasotropic; cerebroprotective; neuroprotective;   |                 |                     |           |             |
| KW        | neotrophic; antibacterial; virucide; fungicide; ophthalmological; human; |                 |                     |           |             |
| KW        | vulnerary; gene therapy. Infection; secreted protein.                    |                 |                     |           |             |
| OS        | Homo sapiens.  |                 |                     |           |             |
| PN        | WO200061623-A1.  |                 |                     |           |             |
| XX        |  |                 |                     |           |             |
| PD        | 19-OCT-2000.   |                 |                     |           |             |
| XX        |  |                 |                     |           |             |
| PF        | 06-APR-2000; 2000WO-US08979.   |                 |                     |           |             |
| XX        |  |                 |                     |           |             |
| PR        | 09-APR-1999; 99US-0128693.   |                 |                     |           |             |
| PR        | 26-APR-1999; 99US-0130991.   |                 |                     |           |             |
| XX        |  |                 |                     |           |             |
| PA        | (HUMA-) HUMAN GENOME SCI INC.  |                 |                     |           |             |
| PI        | Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;              |                 |                     |           |             |
| PI        | Lafleur DM, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;          |                 |                     |           |             |
| PI        | Young PE;  |                 |                     |           |             |
| XX        |  |                 |                     |           |             |
| DR        | WPI. 2000-647418/62.   |                 |                     |           |             |
| XX        |  |                 |                     |           |             |
| XX        | New nucleic acid molecules encoding 62 human secreted proteins for       |                 |                     |           |             |

PT diagnosing, preventing, treating or ameliorating medical conditions and  
 PT used as food additives or preservatives -  
 XX  
 PS Claim 11, Page 643-644; 716pp; English.  
 XX  
 CC Sequences AAB8321-B38396 represent the amino acid sequences of 62  
 CC human secreted proteins encoded by the genes AAC09312-C09587. The genes  
 CC and proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
 CC a range of human tissues disclosed in the specification. The nucleic  
 CC acids, proteins, antibodies and (ant)agonists are useful in the  
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac  
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)  
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)  
 CC infections caused by bacteria, viruses and fungi; and (h) ocular  
 CC disorders e.g. corneal infection. The polypeptides can also be used to  
 CC aid wound healing and epithelial cell proliferation, to prevent skin  
 CC aging due to sunburn, to maintain organs before transplantation, for  
 CC supporting cell culture of primary tissues, to regenerate tissues and in  
 CC chemotaxis.  
 XX  
 XX Sequence 311 AA;  
 SQ  
 Query Match 100.0%; Score 310; DB 21; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-295;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALRRPRLRCARLPDFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCTITTSQT 60  
 Db 1 malrrprrlrcarlpdflillfrgcllgavnlkssnrtpvqefesvelscilttsqt 60  
 QY 61 SDPRIEMKKIODEQTYVFFEDNKIQGDLGRAEILGKTSLKIMWVTRRDSALYCEVVAR 120  
 Db 61 sdpriemkkideqtyvfffnkigdlagraeillgktslikimvtrrdsalyccevar 120  
 QY 121 NDRKEIDEIVELTVQVKPVTVCRAVPVGMATLHCQESGHPRHYSWYRNDVPL 180  
 Db 121 ndrkeideiveltvqkpvtpvcrcvpkavpvgmatlhqeseghprphyswyndvpl 180  
 QY 181 PTDSRANPREFNSSPHLNSGTLVFAVHKDDSGQYYCTASNDAGSARCEQMEYVDL 240  
 Db 181 ptdsramprefnssfhlntsgtlvfaavhkdsgqyyctasndagsarceqemevydl 240  
 QY 241 NIGGILIGVIVLAVLALITLIGICAVYRGYFINNKODGESYKPKGPDGVNYTRTDEG 300  
 Db 241 niggiligvivilavlaalilgiccayrrgyfinnkqdesyknpgkpdgvnytrtdeeg 300  
 QY 301 DFRHKSSFVI 310  
 Db 301 dfrhkssfvil 310  
 RESULT 14  
 AAB80431  
 ID AAB80431 standard; peptide: 339 AA.  
 XX  
 AC AAB80431;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Gene #13 associated peptide #1.  
 XX  
 KM Secreted protein: human; autoimmune; hyperproliferation;  
 KM cardiovascular; cerebrovascular; infection; food.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200107459-A1.  
 XX  
 PD 01-FEB-2001.

XX  
 PF 20-JUL-2000; 2000WO-US19735.  
 XX  
 PR 23-JUL-1999; 99US-0145220.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;  
 PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;  
 DR WPL; 2001-123261/13.  
 XX  
 PT New isolated nucleic acid encoding 29 secreted proteins, for  
 PT diagnosing, preventing and treating e.g. autoimmune,  
 PT hyperproliferative, cardiovascular, and ocular diseases or disorders  
 PT and microorganism infections -  
 XX  
 PS Disclosure; Page 75; 601pp; English.  
 XX  
 CC The present invention relates to 29 human secreted proteins. The  
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid  
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the  
 CC breast or liver, cardiovascular disorders e.g. cardiac arrest,  
 CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,  
 CC nervous system disorders e.g. Alzheimer's disease, infections  
 CC caused by bacteria, viruses and fungi and ocular disorders e.g.  
 CC corneal infection. Also used in food preparations.  
 XX  
 XX Sequence 339 AA;  
 SQ  
 Query Match 100.0%; Score 310; DB 22; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-295;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALRRPRLRCARLPDFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCTITTSQT 60  
 Db 30 malrrprrlrcarlpdflillfrgcllgavnlkssnrtpvqefesvelscilttsqt 89  
 QY 61 SDPRIEMKKIODEQTYVFFEDNKIQGDLGRAEILGKTSLKIMWVTRRDSALYCEVVAR 120  
 Db 90 sdpriemkkideqtyvfffnkigdlagraeillgktslikimvtrrdsalyccevar 149  
 QY 121 NDRKEIDEIVELTVQVKPVTVCRAVPVGMATLHCQESGHPRHYSWYRNDVPL 180  
 Db 150 ndrkeideiveltvqkpvtpvcrcvpkavpvgmatlhqeseghprphyswyndvpl 209  
 QY 181 PTDSRANPREFNSSPHLNSGTLVFAVHKDDSGQYYCTASNDAGSARCEQMEYVDL 240  
 Db 210 ptdsramprefnssfhlntsgtlvfaavhkdsgqyyctasndagsarceqemevydl 269  
 QY 241 NIGGILIGVIVLAVLALITLIGICAVYRGYFINNKODGESYKPKGPDGVNYTRTDEG 300  
 Db 270 niggiligvivilavlaalilgiccayrrgyfinnkqdesyknpgkpdgvnytrtdeeg 329  
 QY 301 DFRHKSSFVI 310  
 Db 330 dfrhkssfvil 339  
 RESULT 15  
 AAY96294  
 ID AAY96294 standard; protein: 310 AA.  
 XX  
 AC AAY96294;  
 XX  
 DT 16-AUG-2000 (first entry)  
 XX  
 DE Human IGFAM-6 immunoglobulin.  
 XX  
 KM Human; immunoglobulin; IGFAM-6; IGFAM; immune disorder; cancer;  
 KM infection; inflammation; haematopoiesis; AIDS; allergy.  
 XX

|                           |  |                              |
|---------------------------|--|------------------------------|
| OS                        |  | Homo sapiens.                |
| XX                        |  |                              |
| FH                        | Key  | Location/Qualifiers          |
| FT                        | Peptide  | 1..30                        |
| FT                        |  | /label- signal_peptide       |
| FT                        | Protein  | 31..310                      |
| FT                        |  | /label- IGFAM-6              |
| FT                        | Domain   | 46..117                      |
| FT                        |  | /label- Ig-domain            |
| FT                        | Domain   | 153..221                     |
| FT                        |  | /label- Ig_domain            |
| FT                        | Domain   | 238..260                     |
| FT                        |  | /label- transmembrane_domain |
| PN                        |  |                              |
| PD                        | WO200029583-A2.  |                              |
| XX                        |  |                              |
| XX                        | 25-MAY-2000.   |                              |
| PF                        |  |                              |
| PE                        | 19-NOV-1999;   | 99WO-US27566.                |
| XX                        |  |                              |
| XX                        | 19-NOV-1998;   | 98US-0113635.                |
| XX                        | 22-DEC-1998;   | 98US-0113635.                |
| PR                        | 07-APR-1999;   | 99US-0128194.                |
| PA                        | (INCY-) INCYTE PHARM INC.  |                              |
| PI                        | Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR:            |                              |
| PI                        | Lu DM, Lal P, Hillman JL, Yang J;  |                              |
| XX                        |  |                              |
| DR                        | WP1; 2000-387796/33.   |                              |
| DR                        | N-PSDB; AAA27386.  |                              |
| PT                        |  |                              |
| PT                        | Immunoglobulin superfamily proteins, the agonist and antagonist of the   |                              |
| PT                        | protein is useful for preventing and treating disorders associated with  |                              |
| PT                        | altered levels of the protein such as cancer, immune system disorders    |                              |
| PS                        | -  |                              |
| PS                        |  |                              |
| PS                        | Claim 1; Page 82-83; 105pp; English.                                     |                              |
| XX                        |  |                              |
| CC                        | The present sequence is the human immunoglobulin superfamily protein     |                              |
| CC                        | IGFAM-6. Its gene was isolated from a cDNA library of leg                |                              |
| CC                        | tissue. It is expressed in reproductive, nervous and                     |                              |
| CC                        | cardiovascular tissue, where cancer and inflammation are common. The     |                              |
| CC                        | gene, protein, its antibodies, agonists and antagonists are suitable for |                              |
| CC                        | diagnosing and treating many diseases, including cancer, immune system   |                              |
| CC                        | disorders (such as inflammation, AIDS, allergies, anaemia,               |                              |
| CC                        | arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's        |                              |
| CC                        | disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,       |                              |
| CC                        | multiple sclerosis, psoriasis), rheumatoid arthritis, scleroderma,       |                              |
| CC                        | systemic lupus erythematosus and ulcerative colitis), complications of   |                              |
| CC                        | cancer, hemodialysis and extracorporeal circulation, trauma and          |                              |
| CC                        | haematopoietic cancer (such as leukaemia) and infections caused by       |                              |
| CC                        | bacteria, viruses, fungi or parasites.                                   |                              |
| SO                        | Sequence   | 310 AA:                      |
| Query Match               | 67.4%; Score 209; DB 21; Length 310;                                     |                              |
| Best Local Similarity     | 99.7%; Pred. No. 1.8e-196;   |                              |
| Matches 309; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;                                       |                              |
| OY                        | 1 MALRRPRLRLCARLPDFLLFRGLCLGAVNLKSSNRPVVOEFSEVELSCIITDSDT 60             |                              |
| Db                        | rrprlrlcarlpdfffflllffgcilgavnlksntprpvgefsvelsciltldsgt 60              |                              |
| OY                        | 61 SPPRIEMWKRTIDEGQTYTFVFNDKTIQGDLAGRAELIGKTSLSLKTWNTTRDSALYRCGVAR 120   |                              |
| Db                        | rrprlrlcarlpdfffflllffgcilgavnlksntprpvgefsvelsciltldsgt 120             |                              |
| OY                        | 121 NNRKEIDEIVIEIYOVQRKVTPVCVRPKPAVPVGKNATTLCOSEGHPRPHYSMYRNDDVL 180     |                              |
| Db                        | ndrkeideivieltyqvkrkvtpvcvcrpkapvpvgkmatlncgeseghpriphyswyrndvpl 180     |                              |

|           |   |   |     |
|-----------|---|---|-----|
| Qy        | 181   | PTRRANDPRFNSSPHLNSFTGLTLPFAVHKDSSGCVYCIASNDMSGARCEOEHEVYDL      | 240 |
| Db        | 181   | pldssamprfnssshlnsetglvtfavhkddsgyyciaandgsasaceeemeyvdl        | 240 |
| Qy        | 241   | NIGGIIGVLVTLVTLVTLITLGIICCAVRRRQYFIRNNQDESEYKRNQKPKDQVNYITFTDEG | 300 |
| Db        | 241   | nlggligvlvltvltvltlclglccayrrgyflnnqdgdesyknpqkpdqynvyltdeeg    | 300 |
| Qy        | 301   | DFRRKSFVYI 310  |     |
| Db        | 301   | dfrkssfvli 310  |     |
| RESULT 16 |   |   |     |
| ID        | AA039254  | standard; Protein: 285 AA.                                      |     |
| XX        | AA039254:   |   |     |
| AC        | AA039254:   |   |     |
| XX        | 02-FEB-2001 (first entry)   |   |     |
| DT        |   |   |     |
| XX        |   |   |     |
| DE        | Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.         |   |     |
| XX        |   |   |     |
| KM        | Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; |   |     |
| KM        | antiproliferative; cytosolic; cardiant; vasotropic; cerebroprotective;    |   |     |
| KM        | nootropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm; |   |     |
| KM        | ophthalmological; autoimmune disease; rheumatoid arthritis; angiogenesis; |   |     |
| KM        | hyperproliferative disorder; cardiovascular disorder; infection;          |   |     |
| KM        | cerebrovascular disorder; nervous system disorder; ocular disorder;       |   |     |
| KM        | wound healing; chemotaxis.  |   |     |
| XX        |   |   |     |
| OS        | Homo sapiens.   |   |     |
| XX        |   |   |     |
| PN        | MO200056754-AL.   |   |     |
| XX        |   |   |     |
| PD        | 28-SEP-2000.  |   |     |
| XX        |   |   |     |
| PF        | 16-MAR-2000; 2000MO-0506792.  |   |     |
| XX        |   |   |     |
| PR        | 19-MAR-1999; 99US-0125362.  |   |     |
| PR        | 10-DEC-1999; 99US-0169980.  |   |     |
| XX        |   |   |     |
| PA        | (HUMA-) HUMAN GENOME SCI INC.   |   |     |
| XX        |   |   |     |
| PI        | Rosen GA, Ruben SM, Komatsoulis G;  |   |     |
| XX        |   |   |     |
| DR        | WPI: 2000-579483/54.  |   |     |
| DR        | N-PSDB: AAC74237.   |   |     |
| XX        |   |   |     |
| PT        | Isolated nucleic acid molecule encoding a human secreted protein is       |   |     |
| XX        | used in preventing, treating or ameliorating a medical condition          |   |     |
| XX        |   |   |     |
| PS        | Disclosure: Page 32; 434pp; English.                                      |   |     |
| XX        |   |   |     |
| CC        | The polynucleotide sequences given in AAC74223-C74279 encode the human    |   |     |
| CC        | secreted proteins represented in AA039179-839226. Sequences               |   |     |
| CC        | AA039227-839308 are alternative proteins encoded by the genes, and also   |   |     |
| CC        | protein sequences with which they share homology. The proteins have       |   |     |
| CC        | activities based on the tissues and cells in which they are expressed.    |   |     |
| CC        | Examples of activities include: immunosuppressive; antiarthritic;         |   |     |
| CC        | antirheumatic; antiproliferative; cytosolic; cardiant; vasotropic;        |   |     |
| CC        | cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;   |   |     |
| CC        | fungicide; and ophthalmological. The human secreted proteins,             |   |     |
| CC        | polynucleotides, antagonists and agonists of the invention may be useful  |   |     |
| CC        | in the treatment, prevention, and/or diagnosis of various disease,        |   |     |
| CC        | disorders and conditions such as autoimmune diseases e.g. rheumatoid      |   |     |
| CC        | arthritis, hyperproliferative disorders e.g. neoplasms of the breast or   |   |     |
| CC        | liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular      |   |     |
| CC        | disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders  |   |     |
| CC        | e.g. Alzheimer's disease, infections caused by bacteria, viruses and      |   |     |
| CC        | fungal and ocular disorders e.g. corneal infection. The polypeptides can  |   |     |
| CC        | also be used to aid wound healing and epithelial cell proliferation, to   |   |     |
| CC        | regenerate tissues, maintain organs before transplantation, in            |   |     |

CC chemotaxis and as a food additive or preservative e.g. to increase  
CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used  
CC during the isolation and characterisation of the genes of the invention.  
XX

SO Sequence 285 AA:

Query Match 51.9%; Score 161; DB 21; Length 285;  
Best Local Similarity 100.0%; Pred. No. 2e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 VVPYKMATLHCQSEGGPRHYSWRNDVLPDPSRANPRRNSFFHLNSETGLVFTAV 209  
Db 125 vpygkmatlhqgeseghprhyswyrndvlpdpsranprrrnsffhl nsetglvftav 184  
QY 210 HKDDSGQYCIASNDAGSARCEOEEMEVYDLNIGITIGVLYVLAVALITLIGCCAYRR 269  
Db 185 hkddsgqyylaandagsarceogemevyl nlgitigvlyvavlaalilgiccayrr 244  
Db 270 GYFINNKQDESYKPNKPGDGVNVRTDEGDERHKSFPVI 310  
245 gyfinnkqdegysknpkpgdgvnyirtdeegdfhksfvl 285

RESULT 17  
ABG04645  
ID ABG04645 standard; Protein; 291 AA.  
XX  
XX ABG04645;  
XX

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #4636.

KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS68832.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity

PS Claim 20: SEQ ID No 35004; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 291 AA:

Query Match 48.7%; Score 151; DB 22; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.3e-139;  
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 DLGRAEILIGKTSIKIWNVTRDSALYRCEVVARNDKEIDEIVIELTVQKPYTPYCRY 146  
Db 134 dlgraelilgktsikimvtrrdsalyrcevarndrkeideiveltvqkpytpcyrr 193  
QY 147 PKAVPYGKMATLHCQSEGGPRHYSWRNDVLPDPSRANPRRNSFFHLNSETGLV 206  
Db 194 pkavpygkmatlhqgeseghprhyswyrndvlpdpsranprrrnsffhl nsetglvf 253  
QY 207 TAVHKDDSGQYCIASNDAGSARCEOEEMEV 237  
Db 254 tavhkddsgqyylaandagsarceogemev 284

RESULT 18  
ABG12109  
ID ABG12109 standard; Protein; 404 AA.  
XX  
XX ABG12109;  
XX

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #12100.

KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS76296.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity

PS Claim 20: SEQ ID No 42468; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The



CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

CC Sequence 404 AA:

Query Match 48.7%; Score 151; DB 22; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-139;  
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 DIAGRAEILGKTSIKIMVTRRDSALYRCEVVARNDKREIDEIVELTVQVPRPVPCRV 146  
 DB 134 diagraeailgktsikimvtrrdsalyrcevarndrkeideiveltvqvpvpcrv 193  
 QY 147 PRAVPVGKMATLHCOESEGPRPHYSWYRNDVPLPTDSRANPRFNSPHLSETGLVF 206  
 DB 194 pravpvgkmatlhcgsegprphyswyndvplptdsranprfnsphlnsetglvf 253  
 QY 207 TAVHRKDSGOYCIASNDGASRCEOEYEV 237  
 DB 254 tavhrkdsqgyctlasndagsarceoev 284

RESULT 19  
 ABG22401  
 ID ABG22401 standard; Protein: 361 AA.  
 XX  
 AC ABG22401;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #22392.  
 XX  
 Human: chromosome mapping; gene mapping; gene therapy; forensics;  
 food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEO INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 DR WPI: 2001-639362/73.  
 DR N-PSDB: AAS86588.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity

XX  
 PS Claim 20: SEQ ID No 52760; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

CC Sequence 361 AA:

Query Match 33.5%; Score 104; DB 22; Length 361;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-93;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 GCLIGAVNLKSSNRTPVVOEFESVELSCIITPDSQSDPRIEMKKIODEQTTFVFFDNKIQ 85  
 DB 35 gcligavnlkssnrtpvvoefesvelscitdsqsdpriemkkidqetvffdnkixq 94  
 QY 86 GDLGRAEILGKTSIKIMVTRRDSALYRCEVVARNDKREIDEI 129  
 DB 95 gdlagraeailgktsikimvtrrdsalyrcevarndrkeidei 138

RESULT 20  
 AAY11472  
 ID AAY11472 standard; Protein: 89 AA.  
 XX  
 AC AAY11472;  
 XX  
 DT 21-JUN-1999 (first entry)  
 XX  
 DE Human 5' EST secreted protein SEQ ID No 294.  
 XX

Human: secreted protein; EST; expressed sequence tag; diagnosis;  
 forensics; gene therapy; chromosome mapping; signal peptide;  
 upstream regulatory sequence; cytokine activity; cell proliferation;  
 differentiation; haematopoiesis regulation; tissue growth regulation;  
 reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;  
 thrombolytic; anti-inflammatory; tumour inhibition.

OS Homo sapiens.  
 XX  
 PN WO9906551-A2.  
 XX  
 PD 11-FEB-1999.  
 XX  
 PF 31-JUL-1998; 98WO-1B01235.  
 PR 01-AUG-1997; 97US-0905133.  
 XX  
 PA (GEST) GENSET.  
 XX  
 PI Duclert A, Dumas Milne Edwards J, Lacroix B;  
 DR WPI: 1999-153781/13.

DR N-PSDB; AAX39538.  
XX New nucleic acids encoding human secreted - proteins obtained from  
PT cDNA libraries prepared from substantia nigra, cerebellum, adrenals  
PT and fetal brain tissue  
XX  
XX Claim 34; Page 394; 434pp; English.  
XX  
CC AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for  
CC human secreted proteins, and encode the proteins given in AAX11374 to  
CC AAX11531, respectively. The proteins given represent the signal peptide  
CC and an N-terminal fragment of a secreted protein. The nucleic acid  
CC sequences can be used for producing secreted human gene products. They  
CC can also be used to develop products for diagnosis and therapy. The  
CC proteins obtained may have cytokine activity, cell  
CC proliferation/differentiation activity, haematopoiesis regulating  
CC activity, tissue growth regulating activity, reproductive hormone  
CC regulating activity, chemotactic/chemokinetic activity, hemostatic and  
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory  
CC activity, tumour inhibition activity or other activities. The products  
CC can be used in forensic, gene therapy and chromosome mapping procedures.  
CC The sequences can also be used for obtaining corresponding promoter  
CC sequences. The nucleic acids encoding of a polypeptide can be used for  
CC directing extracellular secretion of a polypeptide or the insertion of a  
CC polypeptide into a membrane, or importing a polypeptide into a cell.  
XX  
SQ Sequence 89 AA;  
  
Query Match 28 7%; Score 89; DB 20; Length 89;  
Best Local Similarity 100.0%; Pred. No. 2.9e-79;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MALRRPRLRCARLPDFLLFRGCLIGAVNLKSSNRTPVOEFESVESCITTSQT 60  
Db 1 malrrprrlrcarlpdflllfrgcllgavnlkssnrtpvqefesvessclttsqt 60  
  
QY 61 SDPRIEMKKIODEQTYTFEDNKIOGLA 89  
Db 61 sdprlwmkklqdeqtytfvfnkklqgdlia 89  
  
RESULT 21  
ABG27038  
ID ABG27038 standard; Protein; 267 AA.  
XX  
AC ABG27038;  
  
18-FEB-2002 (first entry)  
  
DE Novel human diagnostic protein #27029.  
XX  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
XX WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US08631.  
XX  
XX 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Dirmnac RT, Liu C, Tang YT;  
XX  
XX WPI: 2001-639362/73.  
DR N-PSDB; AAS91225.  
XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
XX Claim 20; SEQ ID No 57397; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 267 AA;  
  
Query Match 20.3%; Score 63; DB 22; Length 267;  
Best Local Similarity 100.0%; Pred. No. 2.3e-53;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 239 DLNIGGTTGGVLYVIALTLTIGCCARRRGYRINNKOGSESKYKNGKPDGVYITDE 298  
Db 130 dlniggttggylyvialtlitgicccarrgyrinnkogseskynkngkpdgvnyitde 189  
  
QY 299 EGD 301  
Db 190 egd 192  
  
RESULT 22  
ABG07157  
ID ABG07157 standard; Protein; 264 AA.  
XX  
AC ABG07157;  
  
13-FEB-2002 (first entry)  
  
DE Novel human diagnostic protein #7148.  
XX  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
XX WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US08631.  
XX  
XX 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Dirmnac RT, Liu C, Tang YT;  
XX  
XX





Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 PRPHYSMYRNDVPLPTDSRANPRF 190  
 |||||  
 Db 167 prphysmyrindvplptdsranprf 190

## RESULT 27

ABB29193  
 ID ABB29193 standard; Peptide; 31 AA.

XX ABB29193;

XX 01-FEB-2002 (first entry)

XX Peptide #1844 encoded by breast cell single exon nucleic acid probe.

XX Human; microarray; single exon probe; gene expression; breast;  
 KM disease; cancer.

XX Homo sapiens.

XX WO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00662.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes,  
 PT useful for measuring gene expression in sample derived from human  
 PT breast, comprises number of single exon nucleic acid probes -

XX Claim 27; SEQ ID NO 12161; 327pp + sequence listing; English.

CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human breast and BT 474 cells. The method involves contacting  
 CC the probes with a collection of detectably labelled nucleic acids  
 CC derived from mRNA of human breast, and then measuring the label  
 CC bound to each probe of the microarray. The probes are useful for  
 CC verifying the expression of regions of genomic DNA predicted to  
 CC encode proteins. They are useful for gene discovery, and for  
 CC determining predisposition and/or prognosing breast disease. Gene  
 CC expression analysis is useful for assessing the toxicity of chemical  
 CC agents on cells. The microarray of this invention presents a far greater  
 CC diversity of probes for measuring gene expression, with far less bias  
 CC than expressed sequence tag microarrays. The method is suitable for  
 CC rapid production of functional information from genomic sequence. The  
 CC present sequence is a peptide encoded by a single exon nucleic acid  
 CC probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 31 AA;

Query Match 2.6%; Score 8; DB 22; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 VLVLAVL 256  
 |||||  
 Db 10 vlvlavl 17

## RESULT 28

ABB34350  
 ID ABB34350 standard; Peptide; 31 AA.

XX ABB34350;

XX 04-FEB-2002 (first entry)

XX Peptide #1856 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human foetal liver -

XX Claim 27; SEQ ID NO 26985; 639pp + sequence listing; English.

CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC foetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 31 AA;

Query Match 2.6%; Score 8; DB 22; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 VLVLAVL 256  
 |||||

Db 10 vlvlavl 17

## RESULT 29

ABB19769  
 ID ABB19769 standard; Protein; 31 AA.

XX ABB19769;

XX 23-JAN-2002 (first entry)  
DT  
XX  
DE Protein #1768 encoded by probe for measuring heart cell gene expression.  
XX  
XX Human; gene expression; heart; microarray; vascular system;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
KW congenital heart disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200157274-A2.  
XX  
PD 09-AUG-2001.  
XX  
PE 30-JAN-2001; 2001WO-US00666.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488899/53.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts -  
XX  
PS Claim 15; SEQ ID No 21539; 530bp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease.  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
SQ  
Sequence 31 AA:  
  
Query Match 2.6%; Score 8; DB 22; Length 31;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 249 VLVLAVL 256  
DB 10 VLVLAVL 17  
  
RESULT 30  
AAM55147  
ID AAM55147 standard; Protein; 31 AA.  
XX  
AC AAM55147;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27252.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe;  
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
PE 30-JAN-2001; 2001WO-US00667.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483446/52.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT brains -  
XX  
PS Example 4; SEQ ID NO: 27252; 650bp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention.  
XX  
SQ  
Sequence 31 AA:  
  
Query Match 2.6%; Score 8; DB 22; Length 31;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 249 VLVLAVL 256  
DB 10 VLVLAVL 17  
  
RESULT 31  
AAM67540  
ID AAM67540 standard; Protein; 31 AA.  
XX  
AC AAM67540;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27846.  
XX  
KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma.  
XX  
OS Homo sapiens.  
XX  
PN WO200157276-A2.  
XX  
PD 09-AUG-2001.  
XX  
PE 30-JAN-2001; 2001WO-US00668.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:39:38 : Search time 23.64 Seconds  
(without alignments)  
320.302 Million cell updates/sec

Title: US-09-524-531C-15

Perfect score: 310  
Sequence: 1 MALRRPRLRLCARLPDFLL.....VNYIRTEDEGDRHRSSEVFI 310

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Hit size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: listing first 75 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUTS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 7     | 2.3         | 14     | 2  | US-08-310-912A-190 |
| 2          | 7     | 2.3         | 14     | 4  | US-09-301-085-190  |
| 3          | 7     | 2.3         | 14     | 5  | PCR-US95-04589-190 |
| 4          | 7     | 2.3         | 52     | 4  | US-09-330-330-9    |
| 5          | 7     | 2.3         | 241    | 1  | US-08-484-227-2    |
| 6          | 7     | 2.3         | 241    | 1  | US-08-476-488-2    |
| 7          | 7     | 2.3         | 241    | 1  | US-08-467-070-2    |
| 8          | 7     | 2.3         | 241    | 1  | US-08-467-070A-2   |
| 9          | 7     | 2.3         | 241    | 5  | PCR-US93-11669-2   |
| 10         | 7     | 2.3         | 244    | 4  | US-08-883-086-9    |
| 11         | 7     | 2.3         | 249    | 2  | US-09-154-807-1    |
| 12         | 7     | 2.3         | 249    | 3  | US-09-373-029-1    |
| 13         | 7     | 2.3         | 333    | 1  | US-08-148-215A-4   |
| 14         | 7     | 2.3         | 454    | 4  | US-09-240-639-11   |
| 15         | 7     | 2.3         | 524    | 2  | US-08-928-692-12   |
| 16         | 7     | 2.3         | 642    | 1  | US-08-706-936-2    |
| 17         | 7     | 2.3         | 642    | 1  | US-08-706-936-3    |
| 18         | 7     | 2.3         | 643    | 2  | US-08-616-844-39   |
| 19         | 7     | 2.3         | 643    | 3  | US-08-599-654-39   |
| 20         | 7     | 2.3         | 643    | 3  | US-08-944-868A-39  |
| 21         | 7     | 2.3         | 643    | 3  | US-08-944-423A-39  |
| 22         | 7     | 2.3         | 643    | 3  | US-08-944-446-39   |
| 23         | 7     | 2.3         | 693    | 1  | US-08-553-279-2    |
| 24         | 7     | 2.3         | 885    | 2  | US-08-310-912A-2   |
| 25         | 7     | 2.3         | 885    | 3  | US-08-841-089-2    |
| 26         | 7     | 2.3         | 885    | 4  | US-09-301-085-2    |
| 27         | 7     | 2.3         | 885    | 5  | PCR-US95-04570-2   |

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|----|---|-----|-------|---|--------------------|--------------------|
| 28 | 7 | 2.3 | 885   | 5 | PCR-US95-04589-2   | Sequence 2, Appl1  |
| 29 | 7 | 2.3 | 907   | 3 | US-08-930-996A-7   | Sequence 7, Appl1  |
| 30 | 7 | 2.3 | 909   | 2 | US-08-310-912A-142 | Sequence 142, App  |
| 31 | 7 | 2.3 | 909   | 4 | US-09-301-085-142  | Sequence 142, App  |
| 32 | 7 | 2.3 | 909   | 5 | PCR-US95-04589-142 | Sequence 142, App  |
| 33 | 7 | 2.3 | 4551  | 3 | US-09-320-878-1    | Sequence 31, Appl1 |
| 34 | 7 | 2.3 | 4613  | 4 | US-09-105-537-31   | Sequence 31, Appl1 |
| 35 | 7 | 2.3 | 11877 | 7 | US-09-105-537-6    | Sequence 80, Appl1 |
| 36 | 6 | 1.9 | 12    | 2 | US-08-406-330-80   | Sequence 80, Appl1 |
| 37 | 6 | 1.9 | 12    | 2 | US-08-556-597-80   | Sequence 80, Appl1 |
| 38 | 6 | 1.9 | 17    | 2 | US-08-321-670-9    | Sequence 9, Appl1  |
| 39 | 6 | 1.9 | 27    | 4 | US-09-227-357-216  | Sequence 276, App  |
| 40 | 6 | 1.9 | 39    | 4 | US-09-220-528-49   | Sequence 49, Appl1 |
| 41 | 6 | 1.9 | 45    | 3 | US-09-053-197A-12  | Sequence 72, Appl1 |
| 42 | 6 | 1.9 | 45    | 4 | US-09-085-761A-17  | Sequence 72, Appl1 |
| 43 | 6 | 1.9 | 50    | 1 | US-08-331-394-12   | Sequence 12, Appl1 |
| 44 | 6 | 1.9 | 50    | 1 | US-08-250-858-12   | Sequence 12, Appl1 |
| 45 | 6 | 1.9 | 50    | 1 | US-08-446-915-12   | Sequence 12, Appl1 |
| 46 | 6 | 1.9 | 50    | 2 | US-08-744-139-12   | Sequence 12, Appl1 |
| 47 | 6 | 1.9 | 50    | 5 | PCR-US95-06639-12  | Sequence 19, Appl1 |
| 48 | 6 | 1.9 | 51    | 2 | US-08-691-814B-19  | Sequence 19, Appl1 |
| 49 | 6 | 1.9 | 76    | 1 | US-08-519-777-22   | Sequence 22, Appl1 |
| 50 | 6 | 1.9 | 76    | 1 | US-08-742-035-22   | Sequence 22, Appl1 |
| 51 | 6 | 1.9 | 76    | 2 | US-08-777-019-22   | Sequence 22, Appl1 |
| 52 | 6 | 1.9 | 76    | 2 | US-08-777-143-22   | Sequence 22, Appl1 |
| 53 | 6 | 1.9 | 76    | 3 | US-08-775-414-22   | Sequence 22, Appl1 |
| 54 | 6 | 1.9 | 76    | 4 | US-08-931-858E-22  | Sequence 22, Appl1 |
| 55 | 6 | 1.9 | 76    | 4 | US-08-981-773-22   | Sequence 22, Appl1 |
| 56 | 6 | 1.9 | 95    | 1 | US-08-519-777-24   | Sequence 24, Appl1 |
| 57 | 6 | 1.9 | 95    | 1 | US-08-742-035-24   | Sequence 24, Appl1 |
| 58 | 6 | 1.9 | 95    | 2 | US-08-777-019-24   | Sequence 24, Appl1 |
| 59 | 6 | 1.9 | 95    | 2 | US-08-777-143-24   | Sequence 24, Appl1 |
| 60 | 6 | 1.9 | 95    | 3 | US-08-775-414-24   | Sequence 24, Appl1 |
| 61 | 6 | 1.9 | 95    | 4 | US-08-931-858E-24  | Sequence 24, Appl1 |
| 62 | 6 | 1.9 | 95    | 4 | US-08-981-773-24   | Sequence 24, Appl1 |
| 63 | 6 | 1.9 | 98    | 1 | US-08-118-270-330  | Sequence 330, App  |
| 64 | 6 | 1.9 | 98    | 5 | PCR-US93-08528-330 | Sequence 330, App  |
| 65 | 6 | 1.9 | 100   | 4 | US-09-230-196-5    | Sequence 5, Appl1  |
| 66 | 6 | 1.9 | 106   | 4 | US-08-936-165A-482 | Sequence 482, App  |
| 67 | 6 | 1.9 | 111   | 4 | US-09-220-528-53   | Sequence 53, Appl1 |
| 68 | 6 | 1.9 | 115   | 2 | US-08-672-345C-18  | Sequence 18, Appl1 |
| 69 | 6 | 1.9 | 115   | 2 | US-08-672-345C-108 | Sequence 108, App  |
| 70 | 6 | 1.9 | 115   | 4 | US-09-214-095D-18  | Sequence 18, Appl1 |
| 71 | 6 | 1.9 | 115   | 4 | US-09-214-095D-98  | Sequence 98, Appl1 |
| 72 | 6 | 1.9 | 119   | 1 | US-08-469-486-49   | Sequence 49, Appl1 |
| 73 | 6 | 1.9 | 119   | 2 | US-08-469-658-49   | Sequence 49, Appl1 |
| 74 | 6 | 1.9 | 123   | 2 | US-08-822-573-2    | Sequence 2, Appl1  |
| 75 | 6 | 1.9 | 145   | 4 | US-09-096-244-2    | Sequence 2, Appl1  |

#### ALIGNMENTS

RESULT 1  
US-08-310-912A-190  
Sequence 190, Application US/08310912A  
Patent No. 5981730  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskawicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Pumiaki  
APPLICANT: Kunkel, Barbara N.  
APPLICANT: Mindrinos, Michael N.  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 208  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston

STATE: MA  
COUNTRY: USA  
ZIP: 02110-2904  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/310,912A  
FILING DATE: September 22, 1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/227,360  
FILING DATE: April 13, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Iech, Karen F.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/254001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 100254  
INFORMATION FOR SEQ. ID NO: 190:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-310-912A-190

Query Match 2.3%; Score 7; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 LALITLG 262  
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Db 5 LALITLG 11

RESULT 2  
US-09-301-085-190  
Sequence 190, Application US/09301085  
Patent No. 6262248  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskiewicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Fumilaki  
APPLICANT: Kunkel, Barbara N.  
APPLICANT: Mindinos, Michael N.  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND  
TITLE OF INVENTION: DETECTION METHODS  
FILE REFERENCE: 00786/254002  
CURRENT APPLICATION NUMBER: US/09/301,085  
CURRENT FILING DATE: 1999-04-28  
EARLIER APPLICATION NUMBER: 08/310,912  
EARLIER FILING DATE: 1994-09-22, 360  
EARLIER APPLICATION NUMBER: 08/227,360  
EARLIER FILING DATE: 1994-04-13  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 190  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-09-301-085-190

Query Match 2.3%; Score 7; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 256 LALITLG 262  
|||||||  
Db 5 LALITLG 11

RESULT 3  
PCT-US95-04589-190  
Sequence 190, Application PC/TUS9504589  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskiewicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Fumilaki  
APPLICANT: Kunkel, Barbara N.  
APPLICANT: Mindinos, Michael N.  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF  
NUMBER OF SEQUENCES: 201  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street Suite 3100  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2904  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04589  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,360  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/230001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 100254  
INFORMATION FOR SEQ ID NO: 190:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-04589-190

Query Match 2.3%; Score 7; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 LALITLG 262  
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Db 5 LALITLG 11

RESULT 4  
US-09-330-330-9  
Sequence 9, Application US/09330330  
Patent No. 6274789  
GENERAL INFORMATION:  
APPLICANT: Yano, Masahito



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:32:32 : Search time 52.83 Seconds  
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651.767 Million cell updates/sec

Title: US-09-524-531c-13

Perfect score: 310

Sequence: 1 MALSRRLRLRLYPHFL.....VNYIRTEGDFRHKSFVI 310

Scoring table:

GAPOP 60.0, Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size: 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database: A.Geneseq.03802.\*

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22: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
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| 1          | 310   | 100.0       | 310    | 21    | Human confuency r  |
| 2          | 310   | 100.0       | 310    | 21    | Murine confuency r |
| 3          | 24    | 7.7         | 285    | 21    | Human secreted pro |
| 4          | 24    | 7.7         | 291    | 22    | Novel human diagno |
| 5          | 24    | 7.7         | 310    | 21    | Human confuency r  |
| 6          | 24    | 7.7         | 310    | 21    | Human PRO1868 prot |
| 7          | 24    | 7.7         | 310    | 21    | PRO1868, an A33 an |
| 8          | 24    | 7.7         | 310    | 21    | Human IGFAM-6 immu |
| 9          | 24    | 7.7         | 310    | 22    | Human polypeptide, |
| 10         | 24    | 7.7         | 310    | 22    | Human polypeptide, |
| 11         | 24    | 7.7         | 310    | 22    | Human PRO1868 poly |

|    |    |     |     |    |                    |
|----|----|-----|-----|----|--------------------|
| 12 | 24 | 7.7 | 310 | 22 | Human PRO1868 prot |
| 13 | 24 | 7.7 | 310 | 22 | Secreted protein e |
| 14 | 24 | 7.7 | 310 | 22 | Secreted protein e |
| 15 | 24 | 7.7 | 310 | 22 | Secreted protein e |
| 16 | 24 | 7.7 | 311 | 21 | Human secreted pro |
| 17 | 24 | 7.7 | 311 | 21 | Human secreted pro |
| 18 | 24 | 7.7 | 311 | 21 | Human secreted pro |
| 19 | 24 | 7.7 | 339 | 22 | Gene #13 associate |
| 20 | 24 | 7.7 | 404 | 22 | Novel human diagno |
| 21 | 21 | 6.8 | 361 | 22 | Novel human diagno |
| 22 | 15 | 4.8 | 68  | 22 | Novel human diagno |
| 23 | 15 | 4.8 | 89  | 20 | Novel human diagno |
| 24 | 10 | 3.2 | 267 | 22 | Novel human diagno |
| 25 | 8  | 2.6 | 48  | 17 | Novel human diagno |
| 26 | 8  | 2.6 | 48  | 17 | Novel human diagno |
| 27 | 8  | 2.6 | 204 | 22 | Novel human diagno |
| 28 | 8  | 2.6 | 204 | 22 | Novel human diagno |
| 29 | 8  | 2.6 | 246 | 19 | Novel human diagno |
| 30 | 8  | 2.6 | 246 | 22 | Novel human diagno |
| 31 | 8  | 2.6 | 324 | 22 | Novel human diagno |
| 32 | 8  | 2.6 | 324 | 22 | Novel human diagno |
| 33 | 8  | 2.6 | 336 | 22 | Novel human diagno |
| 34 | 8  | 2.6 | 506 | 21 | Novel human diagno |
| 35 | 7  | 2.3 | 7   | 21 | Novel human diagno |
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| 45 | 7  | 2.3 | 91  | 22 | Novel human diagno |
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| 48 | 7  | 2.3 | 93  | 22 | Novel human diagno |
| 49 | 7  | 2.3 | 101 | 22 | Novel human diagno |
| 50 | 7  | 2.3 | 104 | 22 | Novel human diagno |
| 51 | 7  | 2.3 | 110 | 21 | Novel human diagno |
| 52 | 7  | 2.3 | 110 | 21 | Novel human diagno |
| 53 | 7  | 2.3 | 111 | 22 | Novel human diagno |
| 54 | 7  | 2.3 | 111 | 22 | Novel human diagno |
| 55 | 7  | 2.3 | 121 | 21 | Novel human diagno |
| 56 | 7  | 2.3 | 127 | 22 | Novel human diagno |
| 57 | 7  | 2.3 | 145 | 21 | Novel human diagno |
| 58 | 7  | 2.3 | 147 | 21 | Novel human diagno |
| 59 | 7  | 2.3 | 147 | 22 | Novel human diagno |
| 60 | 7  | 2.3 | 158 | 21 | Novel human diagno |
| 61 | 7  | 2.3 | 170 | 21 | Novel human diagno |
| 62 | 7  | 2.3 | 170 | 22 | Novel human diagno |
| 63 | 7  | 2.3 | 173 | 22 | Novel human diagno |
| 64 | 7  | 2.3 | 179 | 21 | Novel human diagno |
| 65 | 7  | 2.3 | 180 | 22 | Novel human diagno |
| 66 | 7  | 2.3 | 185 | 22 | Novel human diagno |
| 67 | 7  | 2.3 | 201 | 22 | Novel human diagno |
| 68 | 7  | 2.3 | 208 | 21 | Novel human diagno |
| 69 | 7  | 2.3 | 209 | 22 | Novel human diagno |
| 70 | 7  | 2.3 | 209 | 22 | Novel human diagno |
| 71 | 7  | 2.3 | 233 | 20 | Novel human diagno |
| 72 | 7  | 2.3 | 242 | 22 | Novel human diagno |
| 73 | 7  | 2.3 | 242 | 22 | Novel human diagno |
| 74 | 7  | 2.3 | 242 | 22 | Novel human diagno |
| 75 | 7  | 2.3 | 242 | 22 | Novel human diagno |

#### ALIGNMENTS

RESULT 1  
ID AAB27272 standard: Protein: 310 AA.  
XX

AC AAB27272;  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DE Human confluency regulated adhesion molecule 1 #1.  
 XX  
 KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;  
 KW inflammation; cancer; wound; angiogenesis; human;  
 KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053749-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 13-MAR-2000; 2000WO-EP02219.  
 XX  
 PR 11-MAR-1999; 99EP-0200746.  
 XX  
 (RMFD-) RMF DICTAGENE SA.  
 XX  
 PI Imhof BA, Aurrand-Lions M;  
 XX  
 DR WPI; 2000-587436/55.  
 XX  
 PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or  
 PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation  
 PT reactions and modulating vascular permeability -  
 PS  
 PS Claim 1; Fig 3; 59pp; English.  
 XX  
 CC The present sequence is the human confluency regulated adhesion molecule  
 CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion  
 CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein  
 CC and coding sequence can be used in the treatment of cancer.  
 CC inflammation, to modulate cell-cell interactions and angiogenesis, and  
 CC in the modulation of wound healing.  
 XX  
 SO Sequence 310 AA;

Query Match 100.0%; Score 310; DB 21; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-288;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALSRLRLRLYLARLPHFFLLLRGCMIEAVNLKSSNRNPVHFEFVELSCITTHSQT 60  
 1 malsrlrlrllyarlphffllllfrgcmleavnlkssnrnpvvhfefvelscilthsq 60  
 QY 61 SDPRIEMKKIIDDGOTTYVYPDNKIQGLDAGRTDVFQKTSLRIMWVTRSDSAIYRCEVVAL 120  
 61 sdprlwmkkidggttyvypdnkiqglagrtvdfqktslrilmvtrsdaiyrceval 120  
 DB 61 sdprlwmkkidggttyvypdnkiqglagrtvdfqktslrilmvtrsdaiyrceval 120  
 QY 121 NDREVEDEITELIVQKPVTPVCRIPAAPVPGKTATLQCESEGYRPHYSWRNDVPL 180  
 121 ndreveeditelivqkpvtpvcripaapvpgktatlqcesegyrphyswrvndvpl 180  
 DB 121 ndreveeditelivqkpvtpvcripaapvpgktatlqcesegyrphyswrvndvpl 180  
 QY 181 PTDSRANPRPNSSFHNSETGTLVFNAVHKDSDGYCTIASNDAGAARCGQMEYVDL 240  
 181 ptdsranprpnssfhnsetgtlvfnavhkdsgyctiasndagaarcegdmevydl 240  
 DB 181 ptdsranprpnssfhnsetgtlvfnavhkdsgyctiasndagaarcegdmevydl 240  
 QY 241 NIAGIIGVAVLVILAVITWGTICAYRRCGFISSKODGESYKSPGKHGQVNYRTSEEG 300  
 241 niagiigvavlvilavitwgticayrrcgfisskodgesykpghdgqvnvnyrtseeg 300  
 DB 241 niagiigvavlvilavitwgticayrrcgfisskodgesykpghdgqvnvnyrtseeg 300  
 QY 301 DFRHKSSEFVI 310  
 301 dfrhkssefvi 310  
 DB 301 dfrhkssefvi 310

RESULT 2  
 AAB27278

ID AAB27278 standard; Protein; 310 AA.  
 XX  
 AC AAB27278;  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DE Murine confluency regulated adhesion molecule 1.  
 XX  
 KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;  
 KW inflammation; cancer; wound; angiogenesis; mouse;  
 KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200053749-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 13-MAR-2000; 2000WO-EP02219.  
 XX  
 PR 11-MAR-1999; 99EP-0200746.  
 XX  
 (RMFD-) RMF DICTAGENE SA.  
 XX  
 PI Imhof BA, Aurrand-Lions M;  
 XX  
 DR WPI; 2000-587436/55.  
 DR N-PSDB; AAA97189.  
 XX  
 PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or  
 PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation  
 PT reactions and modulating vascular permeability -  
 PS  
 PS Example; Fig 8; 59pp; English.  
 XX  
 CC The present sequence is the murine confluency regulated adhesion molecule  
 CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion  
 CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein  
 CC and coding sequence can be used in the treatment of cancer. Inflammation,  
 CC to modulate cell-cell interactions and angiogenesis, and in the  
 CC modulation of wound healing.  
 XX  
 SO Sequence 310 AA;

Query Match 100.0%; Score 310; DB 21; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-288;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALSRLRLRLYLARLPHFFLLLRGCMIEAVNLKSSNRNPVHFEFVELSCITTHSQT 60  
 1 malsrlrlrllyarlphffllllfrgcmleavnlkssnrnpvvhfefvelscilthsq 60  
 QY 61 SDPRIEMKKIIDDGOTTYVYPDNKIQGLDAGRTDVFQKTSLRIMWVTRSDSAIYRCEVVAL 120  
 61 sdprlwmkkidggttyvypdnkiqglagrtvdfqktslrilmvtrsdaiyrceval 120  
 DB 61 sdprlwmkkidggttyvypdnkiqglagrtvdfqktslrilmvtrsdaiyrceval 120  
 QY 121 NDREVEDEITELIVQKPVTPVCRIPAAPVPGKTATLQCESEGYRPHYSWRNDVPL 180  
 121 ndreveeditelivqkpvtpvcripaapvpgktatlqcesegyrphyswrvndvpl 180  
 DB 121 ndreveeditelivqkpvtpvcripaapvpgktatlqcesegyrphyswrvndvpl 180  
 QY 181 PTDSRANPRPNSSFHNSETGTLVFNAVHKDSDGYCTIASNDAGAARCGQMEYVDL 240  
 181 ptdsranprpnssfhnsetgtlvfnavhkdsgyctiasndagaarcegdmevydl 240  
 DB 181 ptdsranprpnssfhnsetgtlvfnavhkdsgyctiasndagaarcegdmevydl 240  
 QY 241 NIAGIIGVAVLVILAVITWGTICAYRRCGFISSKODGESYKSPGKHGQVNYRTSEEG 300  
 241 niagiigvavlvilavitwgticayrrcgfisskodgesykpghdgqvnvnyrtseeg 300  
 DB 241 niagiigvavlvilavitwgticayrrcgfisskodgesykpghdgqvnvnyrtseeg 300  
 QY 301 DFRHKSSEFVI 310  
 301 dfrhkssefvi 310  
 DB 301 dfrhkssefvi 310

RESULT 3  
 AAB39254  
 ID AAB39254 standard: Protein: 285 AA.  
 AC AAB39254;  
 DT 02-FEB-2001 (first entry)  
 DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.  
 XX  
 XX Human: secreted protein: immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotrophic; cerebroprotective;  
 KW antiproliferative; cytostatic; cardiant; vasotrophic; cerebroprotective;  
 KW neotropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;  
 KW ophthalmological; autoimmune disease; rheumatoid arthritis; angiogenesis;  
 KW hyperproliferative disorder; cardiovascular disorder; infection;  
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
 KW wound healing; chemotaxis.  
 XX  
 OS Homo sapiens.  
 MO200056754-A1.  
 PD 28-SEP-2000.  
 PF 16-MAR-2000: 2000WO-US06792.  
 PR 19-MAR-1999: 99US-0125362.  
 PR 10-DEC-1999: 99US-0169980.  
 PA (HDMA-) HUMAN GENOME SCI INC.  
 PI Rosen GA, Ruben SM, Komatsoulis G;  
 DR MPI: 2000-579483/54.  
 DR N-PSDB: AAC74237.  
 PT Isolated nucleic acid molecule encoding a human secreted protein is  
 PT used in preventing, treating or ameliorating a medical condition  
 XX  
 PS Disclosure: Page 32; 434pp; English.  
 XX The polynucleotide sequences given in AAC74223-C74279 encode the human  
 CC secreted proteins represented in AAB39179-B39226. Sequences  
 CC AAB39227-B39308 are alternative proteins encoded by the genes, and also  
 CC protein sequences with which they share homology. The proteins have  
 CC activities based on the tissues and cells in which they are expressed.  
 CC Examples of activities include: immunosuppressive; antirheumatic;  
 CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotrophic;  
 CC cerebroprotective; neotropic; neuroprotective; antibacterial; virucide;  
 CC fungicide; and ophthalmological. The human secreted proteins,  
 CC polynucleotides, antagonists and agonists of the invention may be useful  
 CC in the treatment, prevention, and/or diagnosis of various disease,  
 CC disorders and conditions such as autoimmune diseases e.g. rheumatoid  
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders  
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
 CC fungi and ocular disorders e.g. corneal infection. The polypeptides can  
 CC also be used to aid wound healing and epithelial cell proliferation, to  
 CC regenerate tissues, maintain organs before transplantation, in  
 CC chemotaxis and as a food additive or preservative e.g. to increase  
 CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used  
 CC during the isolation and characterisation of the genes of the invention.  
 XX  
 SQ Sequence 285 AA:

Query Match 7.7%; Score 24; DB 21; Length 285;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-14;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 167 PRPHYSWRNDVPLPTDSRANPRF 190

DB 142 prphyswyrndvplptdsranprf 165  
 ||||||||||||||||||||||||||||  
 RESULT 4  
 ABG04645  
 ID ABG04645 standard: Protein: 291 AA.  
 AC ABG04645;  
 DT 13-FEB-2002 (first entry)  
 DE Novel human diagnostic protein #4636.  
 XX  
 XX Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 MO200175067-A2.  
 PD 11-OCT-2001.  
 PF 30-MAR-2001: 2001WO-US08631.  
 PR 31-MAR-2000: 2000US-0540217.  
 PR 23-AUG-2000: 2000US-0649167.  
 PA (HYSE-) HYSEQ INC.  
 PI Drmanac RT, Liu C, Tang YT;  
 DR MPI: 2001-639362/73.  
 DR N-PSDB: AAS68832.  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity  
 XX  
 PS Claim 20; SEQ ID NO 35004; 103pp; English.  
 XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 291 AA:

Query Match 7.7%; Score 24; DB 22; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-14;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 167 PRPHYSWRNDVPLPTDSRANPRF 190  
 ||||||||||||||||||||||||||||

|    |   |
|----|---|
| KW | antiarthralgic; systemic lupus erythematosus; rheumatoid arthritis;     |
| KW | arthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;        |
| KM | idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;      |
| KW | systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  |
| KW | autoimmune thrombocytopenia; immune-mediated renal disease;             |
| KW | demyelinating disease; hepatobiliary disease; Whipple's disease;        |
| KW | inflammatory bowel disease; gluten-sensitive enteropathy;               |
| KW | autoimmune disease; immune-mediated skin disease; allergic disease;     |
| KM | immunological disease; transplantation associated disease;              |
| KW | graft rejection; graft-versus-host-disease.                             |
| OS |   |
| XX | Homo sapiens.   |
| XX |   |
| PN | WO200053758-A2.   |
| PD |   |
| XX | 14-SEP-2000.  |
| PF |   |
| XX | 02-MAR-2000; 2000WO-US05841.  |
| XX |   |
| PR | 08-MAR-1999; 99WO-US05028.  |
| PR | 10-MAR-1999; 99US-0123618.  |
| PR | 12-MAR-1999; 99US-0123957.  |
| PR | 23-MAR-1999; 99US-0125775.  |
| PR | 12-APR-1999; 99US-0128849.  |
| PR | 20-APR-1999; 99WO-US08615.  |
| PR | 28-APR-1999; 99US-0131445.  |
| PR | 04-MAY-1999; 99US-0132371.  |
| PR | 14-MAY-1999; 99US-0134287.  |
| PR | 02-JUN-1999; 99WO-US12252.  |
| PR | 23-JUN-1999; 99US-0141037.  |
| PR | 20-JUL-1999; 99US-0144758.  |
| PR | 26-JUL-1999; 99US-0145689.  |
| PR | 28-JUL-1999; 99US-0146222.  |
| PR | 01-SEP-1999; 99WO-US02011.  |
| PR | 08-SEP-1999; 99WO-US02094.  |
| PR | 13-SEP-1999; 99WO-US20944.  |
| PR | 15-SEP-1999; 99WO-US21090.  |
| PR | 15-SEP-1999; 99WO-US21547.  |
| PR | 05-OCT-1999; 99WO-US23089.  |
| PR | 29-OCT-1999; 99US-0162506.  |
| PR | 29-NOV-1999; 99WO-US28214.  |
| PR | 30-NOV-1999; 99WO-US28313.  |
| PR | 30-NOV-1999; 99WO-US28301.  |
| PR | 01-DEC-1999; 99WO-US28634.  |
| PR | 02-DEC-1999; 99WO-US28551.  |
| PR | 02-DEC-1999; 99WO-US28564.  |
| PR | 02-DEC-1999; 99WO-US28565.  |
| PR | 16-DEC-1999; 99WO-US30095.  |
| PR | 20-DEC-1999; 99WO-US30999.  |
| PR | 30-DEC-1999; 99WO-US31274.  |
| PR | 05-JAN-2000; 2000WO-US00219.  |
| PR | 06-JAN-2000; 2000WO-US00277.  |
| PR | 06-JAN-2000; 2000WO-US00376.  |
| PR | 11-FEB-2000; 2000WO-US03565.  |
| PR | 18-FEB-2000; 2000WO-US04341.  |
| PR | 18-FEB-2000; 2000WO-US04342.  |
| PR | 22-FEB-2000; 2000WO-US04411.  |
| XX |   |
| PA | (GETH ) GENENTECH INC.  |
| XX |   |
| PI | Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W,       |
| PI | Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V,               |
| PI | Stewart TA, Tunas D, Watanabe CK, Wood WI, Yan M;                       |
| XX |   |
| XX | WPI: 2000-572271/53.  |
| DR | N-PSDB: AAC58622.   |
| XX |   |
| PT | Sixty four PRO polypeptides, useful in the diagnosis and treatment of   |
| PT | immune related disorders, e.g. systemic lupus erythematosis, rheumatoid |
| PT | arthritis, osteoarthritis, thyroiditis and diabetes mellitus -          |
| XX |   |
| P5 | Claim 33; Fig 88; 309pp; English  |

XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC8397 to AAC83578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC8579 to AAC8642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

Sequence 310 AA:

Query Match 7.7%; Score 24; DB 21; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 PRPHYSWYRNDVPLPTDSRANPRF 190  
 ||||||||||||||||||||  
 DB 167 PRPHYSWYRNDVPLPTDSRANPRF 190

# RESULT 7

AA96735  
 ID AAY96735 standard; Protein: 310 AA.

XX AAY96735;

DT 26-SEP-2000 (first entry)

XX PRO1868, an A33 antigen homologue.

XX PRO1868; A33 antigen; secreted protein; transmembrane protein;

KW anti-inflammatory; cytostatic; recombinant production; gene therapy.

XX Homo sapiens.

XX

Key Location/Qualifiers  
 Peptide 1..30 /Label= Signal\_peptide

FT Modified-site 26..31 /note= "N-myristoylation site"

FT Modified-site 69..77 /note= "Tyrosine kinase phosphorylation site"

FT Modified-site 104..107 /note= "N-glycosylation site"

FT Modified-site 106..109 /note= "N-glycosylation site"

FT Modified-site 107..110 /note= "Casein kinase II phosphorylation site"

FT Modified-site 107..110 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 192..195 /note= "N-glycosylation site"

FT Modified-site 215..220 /note= "N-glycosylation site"

FT Modified-site 226..231 /note= "N-myristoylation site"

FT Domain 243..263 /note= "N-myristoylation site"

FT Modified-site 243..248 /label= Transmembrane\_domain

FT Modified-site 244..249 /note= "N-myristoylation site"

FT /note= "N-myristoylation site"  
 FT Modified-site 262..267 /note= "N-myristoylation site"  
 FT Modified-site 296..299 /note= "Casein kinase II phosphorylation site"

PD WO200036102-A2.

PD 22-JUN-2000.

PF 01-DEC-1999; 99WO-US28634.

PR 16-DEC-1998; 98US-0112851.

PR 16-DEC-1998; 98US-0113145.

PR 22-DEC-1998; 98US-0113511.

PR 12-JAN-1999; 98US-0115558.

PR 12-JAN-1999; 99US-0115565.

PR 09-FEB-1999; 99US-0115733.

PR 10-FEB-1999; 99US-0119341.

PR 12-FEB-1999; 99US-0119537.

PR 02-JUN-1999; 99US-0119965.

PR 02-JUN-1999; 99WO-US12252.

XX (GERTH ) GENENTECH INC.

XX Borstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;

XX Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;

XX Wood W;

XX WPI: 2000-431586/37.

XX N-PSDB: AAA51265.

XX Isolated nucleic acid molecule encodes a PRO polypeptide which is a

XX transmembrane polypeptide

XX Claim 1: Fig 14; 154pp: English.

XX This is PRO1868, a putative homologue of A33 antigen, a known

XX colorectal cancer-associated marker. The invention concerns novel

XX secreted and transmembrane proteins, designated PRO polypeptides. The

XX cDNA and gene sequences are useful in the recombinant production of PRO

XX polypeptides, as a hybridization probe to screen libraries to isolate

XX cDNAs with sequence identity to PRO polypeptides or to map the gene

XX encoding the PRO polypeptides and analyzing genetic disorders. The

XX cDNA/gene can also be used to produce transgenic animals useful for the

XX development and screening of therapeutically useful reagents. They can

XX also be used in gene therapy, e.g. to replace a defective gene.

XX Sequence 310 AA;

XX

Query Match 7.7%; Score 24; DB 21; Length 310;

Best Local Similarity 100.0%; Pred. No. 1.2e-14; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 PRPHYSWYRNDVPLPTDSRANPRF 190  
 ||||||||||||||||||||

DB 167 PRPHYSWYRNDVPLPTDSRANPRF 190

# RESULT 8

AA96294  
 ID AAY96294 standard; protein: 310 AA.

XX AAY96294;

DT 16-AUG-2000 (first entry)

XX Human IGFAM-6 immunoglobulin.

XX Human: immunoglobulin; IGFAM-6; IGFAM: immune disorder; cancer;

XX Infection; inflammation; haematopoiesis; AIDS; allergy.



PF 07-JUL-2000; 2000EP-0114089.  
 XX 08-JUL-1999; 99JP-0194486.  
 PR 11-JAN-2000; 2000JP-0118774.  
 PR 02-MAY-2000; 2000JP-0183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI: 2001-524255/58.  
 DR N-PSDB: AAK94867.  
 XX  
 PT 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -  
 XX  
 PS Claim 8; SEQ ID NO 4051, 1380bp + sequence listing; English.  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
 CC molecules have been determined. Primers for synthesizing the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a polypeptide  
 CC encoded by a full length human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 CC  
 XX  
 SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 PRPHSWYRNDVPLPTDSRANPRF 190  
 ||||||||||||||||||  
 DB 167 prphswyrndvplptdsranprf 190

RESULT 11  
 AAU12440  
 ID AAU12440 standard; Protein: 310 AA.  
 XX AAU12440;

24-OCT-2001 (first entry)  
 XX Human PRO1868 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 XX adipocyte; A-peptide; factor VIIA; gene therapy.

OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US32678.  
 XX  
 XX 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28651.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 11-FEB-2000; 2000WO-US03376.  
 PR 18-FEB-2000; 2000WO-US03365.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04342.  
 PR 24-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;  
 WPI: 2001-408281/43.  
 DR N-PSDB: AAS21512.

Isolated, secretory and transmembrane PRO polypeptide used to detect  
 other PRO polypeptides. Link bioactive molecules to cells expressing  
 PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 lung, breast, prostate, cervical -

Claim 12; Fig 538; 813pp; English.

AAU12172-AAU12446 represent novel human secretory and transmembrane  
 PRO polypeptides. The PRO polypeptides are useful to detect other  
 PRO polypeptides, to link bioactive molecules to cells expressing  
 PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 polypeptide expression in a cell sample to that in a control sample.  
 Some of the 275 sequences are also useful to stimulate the release of  
 tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 proliferation or differentiation of chondrocytes, the proliferation or  
 gene expression in pericyte cells, the release of proteoglycans from  
 cartilage, the proliferation of inner ear utricular supporting cells or  
 of T-lymphocytes, or the release of a cytokine from peripheral blood  
 monocytes (PMNCs), or the proliferation of endothelial cells. Some of  
 the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 to factor VIIA. The PRO polypeptides can be used in assays to identify  
 molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 XX  
 XX

Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 PRPHSWYRNDVPLPTDSRANPRF 190  
 ||||||||||||||||||  
 DB 167 prphswyrndvplptdsranprf 190

RESULT 12  
 AAB80272

ID AAB80272 standard; Protein; 310 AA.  
 XX  
 AC AAB80272;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Human PRO1668 protein.  
 XX  
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;  
 KW antiparkinsonian nootropic; neuroprotective; vulnereary; cardiac;  
 KW antiangiogenic; vasotropic; antiasthmatic; antihematic; cancer;  
 KW antitubercitic; antinefertility; antidiabetic; antiviral; diabetes;  
 KW ophtalmological; gene therapy; skin disease; gastrointestinal disorder;  
 KW ischaemia; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200104311-A1.  
 XX  
 PE 18-JAN-2001.  
 XX  
 PE 22-FEB-2000; 2000MO-US04414.  
 XX  
 PR 07-JUL-1999; 99US-0143048.  
 XX  
 PR 26-JUL-1999; 99US-0145698.  
 XX  
 PR 28-JUL-1999; 99US-0146222.  
 XX  
 PR 08-SEP-1999; 99MO-US20594.  
 XX  
 PR 13-SEP-1999; 99MO-US20944.  
 XX  
 PR 15-SEP-1999; 99MO-US21090.  
 XX  
 PR 15-SEP-1999; 99MO-US21547.  
 XX  
 PR 05-OCT-1999; 99MO-US23089.  
 XX  
 PR 28-NOV-1999; 99MO-US28214.  
 XX  
 PR 30-NOV-1999; 99MO-US28313.  
 XX  
 PR 16-DEC-1999; 99MO-US30095.  
 XX  
 PR 20-DEC-1999; 99MO-US30911.  
 XX  
 PR 20-DEC-1999; 99MO-US30999.  
 XX  
 PR 05-JAN-2000; 99MO-US00219.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Flivarooff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;  
 PI Mether JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WT;  
 XX  
 DR WPI: 2001-081051/09.  
 XX  
 N-PSDB; AAF72433.  
 XX  
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in  
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung  
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.  
 PT Alzheimer's disease) -  
 XX  
 PS Claim 1; Fig 124; 393pp; English.  
 XX  
 CC The present sequence is one of sixty one novel secreted and  
 CC transmembrane PRO polypeptides. The PRO polypeptides are  
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.  
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,  
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.  
 CC endometrial bleeding, angiogenesis, ischaemias such as coronary  
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,  
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and  
 CC diabetes and retinal disorders such as retinitis pigmentosum.  
 CC The PRO nucleic acids have applications in molecular biology, including  
 CC use as hybridization probes, and in chromosome and gene mapping.  
 XX  
 SO Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;

Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 167 PRPHYSWRNDVPLPTDSRANPR 190  
 ||||||||||||||||||||||||||||  
 Db 167 PRPHYSWRNDVPLPTDSRANPR 190  
 RESULT 13  
 AAB80383  
 ID AAB80383 standard; protein; 310 AA.  
 XX  
 AC AAB80383;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Secreted protein encoded by gene #13.  
 XX  
 KW Secreted protein; human; autoimmune; hyperproliferation;  
 KW cardiovascular; cerebrovascular; infection; food.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200107459-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PE 20-JUL-2000; 2000MO-US19735.  
 XX  
 PR 23-JUL-1999; 99US-0145220.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;  
 PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;  
 XX  
 DR WPI: 2001-123261/13.  
 XX  
 PT New isolated nucleic acid encoding 29 secreted proteins, for  
 PT diagnosing, preventing and treating e.g. autoimmune,  
 PT hyperproliferative, cardiovascular, and ocular diseases or disorders  
 PT and microorganism infections -  
 XX  
 PS Claim 11; Page 538-539; 601pp; English.  
 XX  
 CC The present invention relates to 29 human secreted proteins. The  
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid  
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the  
 CC breast or liver, cardiovascular disorders e.g. cardiac arrest,  
 CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,  
 CC nervous system disorders e.g. Alzheimer's disease, infections  
 CC caused by bacteria, viruses and fungi and ocular disorders e.g.  
 CC corneal infection. Also used in food preparations.  
 XX  
 SO Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 167 PRPHYSWRNDVPLPTDSRANPR 190  
 ||||||||||||||||||||||||||||  
 Db 167 PRPHYSWRNDVPLPTDSRANPR 190  
 RESULT 14  
 AAB80408  
 ID AAB80408 standard; protein; 310 AA.  
 XX  
 AC AAB80408;  
 XX  
 DT 24-APR-2001 (first entry)



[illegible][illegible]

XX Claim 11; Page 603-604; 716pp; English.  
XX Sequences AAB38321-B38396 represent the amino acid sequences of 62  
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes  
CC and proteins are useful for preventing, ameliorating or treating medical  
CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
CC a range of human tissues disclosed in the specification. The nucleic  
CC acids, proteins, antibodies and (ant)agonists are useful in the  
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac  
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)  
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)  
CC infections caused by bacteria, viruses and fungi; and (h) ocular  
CC disorders e.g. corneal infection. The polypeptides can also be used to  
CC aid wound healing and epithelial cell proliferation, to prevent skin  
CC aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis.

SQ Sequence 311 AA:

Query Match 7.7%; Score 24; DB 21; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190  
DB 167 prphyswyrndvplptdsranprf 190  
|||||

RESULT 17

AAB38383  
ID AAB38383 standard; Protein; 311 AA.

AC AAB38383;

DT 31-JAN-2001 (first entry)

DE Human secreted protein encoded by gene 13 clone HAPSA79.

XX Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;  
KW cytostatic; cardiact; vasotropic; cerebroprotective; neuroprotective;  
KW cytotoxic; antibacterial; virucide; fungicide; optalmallogical; human;  
KW vulnerary; gene therapy; infection; secreted protein.

Homo sapiens.

PN WO200061623-A1.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US08979.

PR 09-APR-1999; 99US-0128693.

PR 26-APR-1999; 99US-0130991.

PA (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;  
PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;  
PI Young PE;

WPI; 2000-647418/62.

XX New nucleic acid molecules encoding 62 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
PT used as food additives or preservatives -  
XX Claim 11; Page 642-643; 716pp; English.

CC Sequences AAB38321-B38396 represent the amino acid sequences of 62  
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes  
CC and proteins are useful for preventing, ameliorating or treating medical  
CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
CC a range of human tissues disclosed in the specification. The nucleic  
CC acids, proteins, antibodies and (ant)agonists are useful in the  
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac  
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)  
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)  
CC infections caused by bacteria, viruses and fungi; and (h) ocular  
CC disorders e.g. corneal infection. The polypeptides can also be used to  
CC aid wound healing and epithelial cell proliferation, to prevent skin  
CC aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis.

SQ Sequence 311 AA:

Query Match 7.7%; Score 24; DB 21; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190  
DB 167 prphyswyrndvplptdsranprf 190  
|||||

RESULT 18

AAB38384  
ID AAB38384 standard; Protein; 311 AA.

AC AAB38384;

DT 31-JAN-2001 (first entry)

DE Human secreted protein encoded by gene 13 clone HAPSA79.

XX Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;  
KW cytostatic; cardiact; vasotropic; cerebroprotective; neuroprotective;  
KW cytotoxic; antibacterial; virucide; fungicide; optalmallogical; human;  
KW vulnerary; gene therapy; infection; secreted protein.

Homo sapiens.

PN WO200061623-A1.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US08979.

PR 09-APR-1999; 99US-0128693.

PR 26-APR-1999; 99US-0130991.

XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;  
PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;  
PI Young PE;

WPI; 2000-647418/62.

XX New nucleic acid molecules encoding 62 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
PT used as food additives or preservatives -  
XX Claim 11; Page 643-644; 716pp; English.

XX Sequences AAB38321-B38396 represent the amino acid sequences of 62  
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes  
CC and proteins are useful for preventing, ameliorating or treating medical

CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
CC a range of human tissues disclosed in the specification. The nucleic  
CC acids, proteins, antibodies and (ant)agonists are useful in the  
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac  
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)  
CC angiodysplasia; (f) nervous system disorders e.g. Alzheimer's disease; (g)  
CC infections caused by bacteria, viruses and fungi; and (h) ocular  
CC disorders e.g. corneal infection. The polypeptides can also be used to  
CC aid wound healing and epithelial cell proliferation, to prevent skin  
CC aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis.

XX SQ Sequence 311 AA;

Query Match 7.7%; Score 24; DB 21; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 167 PRPHSWRNVDVLPDSTRANPRF 190  
|||||  
DB 167 prphswyrndvlpdstranprf 190

RESULT 19  
AAB80431  
ID AAB80431 standard: peptide: 339 AA.  
XX AAB80431;  
XX 24-APR-2001 (first entry)  
XX DE Gene #13 associated peptide #1.  
XX KW Secreted protein; human; autoimmune; hyperproliferation;  
XX KW cardiovascular; cerebrovascular; infection; food.  
XX OS Homo sapiens.  
XX PN WO200107459-A1.  
XX PD 01-FEB-2001.  
XX PF 20-JUL-2000; 2000WO-US19735.  
XX PE 23-JUL-1999; 99US-0145220.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;  
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsu GA;  
XX WPI: 2001-123261/13.  
XX DR  
XX PT New isolated nucleic acid encoding 29 secreted proteins, for  
PT diagnosing, preventing and treating e.g. autoimmune,  
PT hyperproliferative, cardiovascular, and ocular diseases or disorders  
PT and microorganism infections  
XX PS  
XX Disclosure: Page 75; 601pp; English.  
XX The present invention relates to 29 human secreted proteins. The  
XX invention is used to prevent autoimmune diseases e.g. rheumatoid  
XX arthritis, hyperproliferative disorders e.g. neoplasms of the  
XX breast or liver, cardiovascular disorders e.g. cardiac arrest,  
XX cerebrovascular disorders e.g. cerebral ischemia, angiodysplasia,  
XX nervous system disorders e.g. Alzheimer's disease, infections  
XX caused by bacteria, viruses and fungi and ocular disorders e.g.  
XX corneal infection. Also used in food preparations.

SQ Sequence 339 AA;

Query Match 7.7%; Score 24; DB 22; Length 339;  
Best Local Similarity 100.0%; Pred. No. 1.3e-14;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 167 PRPHSWRNVDVLPDSTRANPRF 190  
|||||  
DB 196 prphswyrndvlpdstranprf 219

RESULT 20  
ABG12109  
ID ABG12109 standard: Protein; 404 AA.  
XX ABG12109;  
XX 18-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #12100.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US08631.  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX PA (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI: 2001-639362/73.  
XX DR N-PSDB; AAS76296.  
XX PD  
XX PF  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX PS  
XX Claim 20; SEQ ID No 42468; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence  
XX tags for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to restore normal activity of (II) or to treat disease states involving  
XX (II). (II) is useful for generating antibodies against it, detecting or  
XX quantitating a polypeptide in tissue, as molecular weight markers and as  
XX a food supplement. (II) and its binding partners are useful in medical  
XX imaging of sites expressing (II). (I) and (II) are useful for treating  
XX disorders involving aberrant protein expression or biological activity.  
XX The polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. ABG00010-ABG30377 represent novel human  
XX diagnostic amino acid sequences of the invention.  
XX Note: The sequence data for this patent did not appear in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 404 AA;







Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 252 VLVIVAVI 259  
 |||||  
 Db 1 VLVIVAVI 8

RESULT 27  
 AAG81659  
 ID AAG81659 standard; Protein; 204 AA.  
 XX  
 AC AAG81659;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE S. epidermidis open reading frame protein sequence SEQ ID NO:412.  
 XX  
 KW Staphylococcus epidermidis SRI strain; infection; diagnosis;  
 KM vaccination; endocarditis.  
 XX  
 XX Staphylococcus epidermidis.  
 XX  
 FN WO200134809-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PF 09-NOV-2000; 2000WO-US30782.  
 XX  
 PR 09-NOV-1999; 99US-0164258.  
 XX  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Kimerly MJ;  
 XX  
 DR WPI: 2001-316495/33.  
 XX  
 DR N-PSDB; AAH52509.  
 XX  
 PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
 PS useful for vaccinating against infections, e.g. endocarditis -  
 XX  
 PS Claim 18; Page 151; 2188pp; English.

CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.  
 CC (I) and (II) can have antibacterial activity and therefore can be used  
 CC in vaccination. The nucleic acids (I) may be used to produce the  
 CC S. epidermidis polypeptides (II) via the production of vectors  
 CC containing them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH5090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH5091 to  
 CC AAH5098 represent oligonucleotide sequences and primers which are used  
 CC in the exemplification of the present invention.  
 CC N.B. The present invention specifically claims all the polynucleotide  
 CC sequences given in the sequence listing of the present specification,  
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
 CC no sequences are present for SEQ ID NO:4455 to 4464.  
 XX  
 SQ Sequence 204 AA;

Query Match 2.6%; Score 8; DB 22; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 IAGIIGGV 249  
 |||||  
 Db 181 IAGIIGGV 188

RESULT 28  
 AAG82062  
 ID AAG82062 standard; Protein; 204 AA.  
 XX  
 AC AAG82062;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE S. epidermidis open reading frame protein sequence SEQ ID NO:1218.  
 XX  
 KW Staphylococcus epidermidis SRI strain; infection; diagnosis;  
 KM vaccination; endocarditis.  
 XX  
 OS Staphylococcus epidermidis.  
 XX  
 PN WO200134809-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PF 09-NOV-2000; 2000WO-US30782.  
 XX  
 PR 09-NOV-1999; 99US-0164258.  
 XX  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Kimerly MJ;  
 XX  
 DR WPI: 2001-316495/33.  
 XX  
 DR N-PSDB; AAH52912.  
 XX  
 PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
 PS useful for vaccinating against infections, e.g. endocarditis -  
 XX  
 PS Claim 18; Page 349; 2188pp; English.

CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.  
 CC (I) and (II) can have antibacterial activity and therefore can be used  
 CC in vaccination. The nucleic acids (I) may be used to produce the  
 CC S. epidermidis polypeptides (II) via the production of vectors  
 CC containing them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH5090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH5091 to  
 CC AAH5098 represent oligonucleotide sequences and primers which are used  
 CC in the exemplification of the present invention.  
 CC N.B. The present invention specifically claims all the polynucleotide  
 CC sequences given in the sequence listing of the present specification,  
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
 CC no sequences are present for SEQ ID NO:4455 to 4464.  
 XX  
 SQ Sequence 204 AA;

Query Match 2.6%; Score 8; DB 22; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 IAGIIGGV 249  
 |||||  
 Db 181 IAGIIGGV 188

RESULT 29  
 AAW41974  
 ID AAW41974 standard; Protein; 246 AA.

```

XX AC AAM41974;
XX XX
XX 02-JUL-1998 (first entry)
XX XX
DE Flea serine protease SEQ ID NO:129.
XX XX
XX Flea; Siphonaptera; protease; vaccine; prophylaxis; infestation;
XX KM Immunoglobulin protease; larvae; host animal.
XX OS Siphonaptera.
XX FH Key Location/Qualifiers
XX FT Misc-difference 241
XX FT /note= "encoded by TAA, a stop codon"
XX PN WO9740058-A1.
XX XX
XX 30-OCT-1997.
XX XX
XX 24-APR-1997; 97WO-0506121.
XX XX
XX 04-APR-1997; 97US-0042945.
XX PR 24-APR-1996; 96US-0639075.
XX PR 15-NOV-1996; 96US-0749699.
XX XX
XX (HESK-) HESKA CORP.
XX XX
XX Frank GR, Gaines PJ, Grievie RB, Hunter SM, Rushlow KE;
XX PI Silver G, Stiegler GL;
XX XX
XX WPI; 1998-076762/07.
XX DR N-PSDB; AAV04597.
XX XX
XX New flea protease genes and proteins - used in vaccine compositions
XX PT for the prophylaxis and treatment of flea infestation, especially in
XX PT cats or dogs
XX XX
XX Claim 2; Page 260-261; 318pp; English.
XX XX
XX The present sequence represents a novel flea serine protease. The
XX CC protease, its mimetopes, antibodies (Ab) and inhibitors of the
XX CC protein, as well as the DNA encoding the protein, may all be used in
XX CC therapeutic compositions to reduce flea protease activity (especially
XX CC immunoglobulin protease) and so reduce flea infestation, especially in
XX CC cats or dogs. Alternatively, flea larvae may ingest the faeces of adult
XX CC fleas which comprises anti-protease antibodies produced by a host animal
XX CC in response to administration of the protein. Therapeutic compositions
XX CC may further comprise a compound that reduces haematophagous ectoparasite
XX CC burden by a method other than by reducing flea immunoglobulin protease
XX CC activity. The novel flea DNA encoding the protein can also be used to
XX CC produce recombinant protein, and fragments of it are used as probes and
XX CC primers for identification and isolation of related sequences, also as
XX CC antisense, triplex-forming agents and ribozymes for inhibition of the
XX CC synthesis of the protein. Ab are also useful for screening expression
XX CC libraries, to purify the protein and to target cytotoxins to fleas.
XX XX
XX Sequence 246 AA;
XX

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Query Match 2.6%; Score 8; DB 19; Length 246;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 252 VLIIVLAVI 259
DB 2 vliivlavi 9

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RESULT 30
AAB50616
ID AAB50616 standard; Protein: 246 AA.
XX

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AC AAB50616;
XX XX
XX 19-MAR-2001 (first entry)
XX XX
DE Flea serine protease PfSP12-246 protein sequence #127.
XX XX
XX Flea; cat flea; serine protease; aminopeptidase; cysteine protease;
XX KM flea infestation; proteolytic; insecticide; vaccine; cat; dog; flea;
XX KM Ctenocephalides felis; Ctenocephalides canis; Pulex irritans;
XX KM ectoparasite.
XX XX
XX Ctenocephalides felis.
XX OS
XX US6150125-A.
XX PN
XX 21-NOV-2000.
XX PD
XX 24-APR-1996; 96US-0639075.
XX PF
XX 13-DEC-1991; 91US-0806482.
XX PR 18-OCT-1994; 94US-0326773.
XX PR 07-JUN-1995; 95US-0482130.
XX PR 07-JUN-1995; 95US-0484211.
XX PR 07-JUN-1995; 95US-0485443.
XX PR 07-JUN-1995; 95US-0485455.
XX PR 15-AUG-1997; 97WO-0514442.
XX XX
XX (HESK-) HESKA CORP.
XX XX
XX Gaines PJ, Silver G, Rushlow KE, Hunter SM, Frank GR, Stiegler GL;
XX PI Grievie RB;
XX XX
XX WPI; 2001-136374/14.
XX DR N-PSDB; AAC90878.
XX XX
XX New isolated flea proteins with proteolytic activity, useful for
XX PT preventing and reducing flea infestations in mammals especially cats
XX PT and dogs -
XX XX
XX Claim 1; Column 195-198; 150pp; English.
XX PS
XX XX
XX The present invention describes isolated flea serine protease,
XX CC aminopeptidase and cysteine protease proteins (I). Also described is a
XX CC method for identifying a compound (II) capable of inhibiting flea
XX CC protease activity comprising: (a) contacting (I) with a protease
XX CC substrate and a putative inhibitory compound, where (I) has proteolytic
XX CC activity in the absence of the compound; and (b) determining if the
XX CC compound inhibits protease activity by detecting cleavage of the
XX CC protease substrates; where decreased cleavage of the protease substrate
XX CC indicates an inhibitory compound. (I), nucleic acid molecules encoding
XX CC (I), and antibodies immunospecific for (I) and (II) are useful for
XX CC preventing and reducing flea infestations, particularly the species
XX CC Ctenocephalides felis (cat fleas), Ctenocephalides canis (dog fleas) and
XX CC Pulex irritans, in animals, preferably cats and dogs. They are also
XX CC useful for reducing infestation by other ectoparasites, preferably
XX CC mosquitoes, midges, sandflies, blackflies, ticks and Rhodnius. AAC90818
XX CC to AAC90913 and AAB50551 to AAB50844 represent sequences used in the
XX CC exemplification of the present invention.
XX XX
XX Sequence 246 AA;
XX

```

```

Query Match 2.6%; Score 8; DB 22; Length 246;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 252 VLIIVLAVI 259
DB 2 vliivlavi 9

```

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RESULT 31
AAC93112

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:32:47 : Search time 23.64 Seconds  
(without alignments)  
320.302 Million cell updates/sec

Title: US-09-524-531C-13

Perfect score: 310

Sequence: 1 MALSRRLRLRLVRLPFL.....VNYIRTEGDFRHKSSFVI 310

Scoring table:

OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Hit size: 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database:

Issued\_Patents\_AA:  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
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| 1          | 8     | 2.6         | 48     | 1  | US-08-485-455D-65  |
| 2          | 8     | 2.6         | 48     | 2  | US-08-482-130C-65  |
| 3          | 8     | 2.6         | 48     | 2  | US-08-484-211C-65  |
| 4          | 8     | 2.6         | 48     | 3  | US-08-906-769-65   |
| 5          | 8     | 2.6         | 48     | 3  | US-08-906-616-65   |
| 6          | 8     | 2.6         | 48     | 4  | US-08-817-795-65   |
| 7          | 8     | 2.6         | 48     | 4  | US-08-485-443B-65  |
| 8          | 8     | 2.6         | 48     | 4  | US-08-639-075A-65  |
| 9          | 8     | 2.6         | 48     | 4  | US-09-012-431-65   |
| 10         | 8     | 2.6         | 48     | 4  | US-09-012-692-65   |
| 11         | 8     | 2.6         | 48     | 4  | US-08-906-613-65   |
| 12         | 8     | 2.6         | 48     | 5  | PCT-US95-14442A-65 |
| 13         | 8     | 2.6         | 246    | 3  | US-08-906-769-127  |
| 14         | 8     | 2.6         | 246    | 3  | US-08-906-616-127  |
| 15         | 8     | 2.6         | 246    | 4  | US-08-639-075A-127 |
| 16         | 8     | 2.6         | 246    | 4  | US-09-012-431-127  |
| 17         | 8     | 2.6         | 246    | 4  | US-09-012-692-127  |
| 18         | 8     | 2.6         | 246    | 4  | US-08-906-613-127  |
| 19         | 8     | 2.3         | 170    | 3  | US-09-188-035-2    |
| 20         | 7     | 2.3         | 170    | 4  | US-09-382-086-2    |
| 21         | 7     | 2.3         | 249    | 2  | US-09-154-802-1    |
| 22         | 7     | 2.3         | 249    | 3  | US-09-373-029-1    |
| 23         | 7     | 2.3         | 758    | 4  | US-09-413-814-32   |
| 24         | 7     | 2.3         | 775    | 1  | US-07-603-133B-15  |
| 25         | 7     | 2.3         | 775    | 1  | US-07-603-133B-16  |
| 26         | 7     | 2.3         | 1186   | 2  | US-08-861-464-8    |
| 27         | 7     | 2.3         | 1186   | 2  | US-08-396-001-8    |

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| 28 | 7 | 2.3 | 1186 | 4 | US-09-323-433A-8   | Sequence 8, Appl1  |
| 29 | 7 | 2.3 | 1395 | 4 | US-09-540-245A-15  | Sequence 15, Appl1 |
| 30 | 6 | 1.9 | 14   | 2 | US-08-685-589A-164 | Sequence 164, App  |
| 31 | 6 | 1.9 | 27   | 4 | US-09-227-357-276  | Sequence 276, App  |
| 32 | 6 | 1.9 | 29   | 1 | US-07-960-510-4    | Sequence 4, Appl1  |
| 33 | 6 | 1.9 | 29   | 1 | US-07-960-510-5    | Sequence 5, Appl1  |
| 34 | 6 | 1.9 | 29   | 1 | US-07-960-510-6    | Sequence 6, Appl1  |
| 35 | 6 | 1.9 | 29   | 1 | US-07-960-510-7    | Sequence 7, Appl1  |
| 36 | 6 | 1.9 | 35   | 6 | 5171673-7          | Patent No. 5171673 |
| 37 | 6 | 1.9 | 45   | 3 | US-09-053-197A-72  | Sequence 72, Appl1 |
| 38 | 6 | 1.9 | 45   | 3 | US-09-085-761A-77  | Sequence 77, Appl1 |
| 39 | 6 | 1.9 | 48   | 1 | US-07-796-361A-15  | Sequence 15, Appl1 |
| 40 | 6 | 1.9 | 93   | 1 | US-08-591-498-1    | Sequence 1, Appl1  |
| 41 | 6 | 1.9 | 115  | 2 | US-08-672-345C-18  | Sequence 18, Appl1 |
| 42 | 6 | 1.9 | 115  | 2 | US-08-672-345C-108 | Sequence 108, App  |
| 43 | 6 | 1.9 | 115  | 4 | US-09-214-095D-18  | Sequence 18, Appl1 |
| 44 | 6 | 1.9 | 115  | 4 | US-09-214-095D-98  | Sequence 98, Appl1 |
| 45 | 6 | 1.9 | 123  | 2 | US-08-822-573-2    | Sequence 2, Appl1  |
| 46 | 6 | 1.9 | 132  | 1 | US-08-591-498-16   | Sequence 16, Appl1 |
| 47 | 6 | 1.9 | 145  | 1 | US-09-096-244-2    | Sequence 2, Appl1  |
| 48 | 6 | 1.9 | 158  | 2 | US-08-846-762-2    | Sequence 2, Appl1  |
| 49 | 6 | 1.9 | 208  | 2 | US-08-700-607-7    | Sequence 7, Appl1  |
| 50 | 6 | 1.9 | 219  | 1 | US-08-441-629-13   | Sequence 13, Appl1 |
| 51 | 6 | 1.9 | 219  | 3 | US-08-776-207-13   | Sequence 13, Appl1 |
| 52 | 6 | 1.9 | 219  | 5 | PCT-US95-09172-13  | Sequence 27, Appl1 |
| 53 | 6 | 1.9 | 228  | 2 | US-08-417-495-27   | Sequence 27, Appl1 |
| 54 | 6 | 1.9 | 228  | 2 | US-08-284-391B-27  | Sequence 27, Appl1 |
| 55 | 6 | 1.9 | 228  | 4 | US-09-218-950-27   | Sequence 27, Appl1 |
| 56 | 6 | 1.9 | 228  | 5 | PCT-US92-01785-27  | Sequence 27, Appl1 |
| 57 | 6 | 1.9 | 228  | 5 | PCT-US95-00454-27  | Sequence 27, Appl1 |
| 58 | 6 | 1.9 | 236  | 3 | US-08-705-771-19   | Sequence 19, Appl1 |
| 59 | 6 | 1.9 | 235  | 3 | US-08-906-769-91   | Sequence 91, Appl1 |
| 60 | 6 | 1.9 | 255  | 3 | US-08-906-616-91   | Sequence 91, Appl1 |
| 61 | 6 | 1.9 | 255  | 4 | US-08-817-795-91   | Sequence 91, Appl1 |
| 62 | 6 | 1.9 | 255  | 4 | US-08-639-075A-91  | Sequence 91, Appl1 |
| 63 | 6 | 1.9 | 255  | 4 | US-09-012-431-91   | Sequence 91, Appl1 |
| 64 | 6 | 1.9 | 255  | 4 | US-09-012-692-91   | Sequence 91, Appl1 |
| 65 | 6 | 1.9 | 255  | 4 | US-08-906-613-91   | Sequence 91, Appl1 |
| 66 | 6 | 1.9 | 255  | 5 | PCT-US95-14442A-91 | Sequence 91, Appl1 |
| 67 | 6 | 1.9 | 265  | 2 | US-08-807-044-1    | Sequence 1, Appl1  |
| 68 | 6 | 1.9 | 266  | 6 | 5175383-5          | Patent No. 5175383 |
| 69 | 6 | 1.9 | 267  | 1 | US-08-462-169B-13  | Sequence 13, Appl1 |
| 70 | 6 | 1.9 | 267  | 2 | US-08-700-607-8    | Sequence 8, Appl1  |
| 71 | 6 | 1.9 | 267  | 3 | US-09-103-079-13   | Sequence 13, Appl1 |
| 72 | 6 | 1.9 | 268  | 1 | US-08-439-725A-12  | Sequence 12, Appl1 |
| 73 | 6 | 1.9 | 268  | 1 | US-08-464-590A-17  | Sequence 17, Appl1 |
| 74 | 6 | 1.9 | 268  | 2 | US-08-207-412B-12  | Sequence 12, Appl1 |
| 75 | 6 | 1.9 | 268  | 2 | US-08-867-471-12   | Sequence 12, Appl1 |

#### ALIGNMENTS

RESULT 1  
US-08-485-455D-65  
Sequence 65, Application US/08485455D  
Patent No. 51712143  
GENERAL INFORMATION:  
APPLICANT: Grieve, Robert B.  
APPLICANT: Rushlow, Keith E.  
APPLICANT: Wu Hunter, Shirley  
APPLICANT: Frank, Glenn R.  
APPLICANT: Stiegler, Gary L.  
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID  
NUMBER OF INVENTION: 79  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sheridan Ross P.C.  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80203

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,455D  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-25-C1-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-455D-65

Query Match 2.6%; Score 8; DB 1; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 252 VLIYLA VI 259  
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Db 1 VLIYLA VI 8

RESULT 2  
US-08-482-130C-65  
Sequence 65, Application US/08482130C  
Patent No. 5962257  
GENERAL INFORMATION:  
APPLICANT: Grieve, Robert B.  
APPLICANT: Rushlow, Keith E.  
APPLICANT: Wu Hunter, Shirley  
APPLICANT: Frank, Glenn R.  
APPLICANT: Stiegler, Gary L.  
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID  
TITLE OF INVENTION: MOLECULES, AND USES THEREOF  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross P.C.  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,130C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-25-C1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-130C-65

Query Match 2.6%; Score 8; DB 2; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 252 VLIYLA VI 259  
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Db 1 VLIYLA VI 8

RESULT 3  
US-08-484-211C-65  
Sequence 65, Application US/08484211C  
Patent No. 5972645  
GENERAL INFORMATION:  
APPLICANT: Grieve, Robert B.  
APPLICANT: Rushlow, Keith E.  
APPLICANT: Wu Hunter, Shirley  
APPLICANT: Frank, Glenn R.  
APPLICANT: Stiegler, Gary L.  
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID  
TITLE OF INVENTION: MOLECULES, AND USES THEREOF  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross P.C.  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,211C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-25-C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-211C-65

Query Match 2.6%; Score 8; DB 2; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 252 VLIYLA VI 259  
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Db 1 VLIYLA VI 8

RESULT 4  
US-08-906-769-65  
Sequence 65, Application US/08906769  
Patent No. 6077687

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:33:22 ; Search time 30.81 Seconds

(without alignments)  
966.819 Million cell updates/sec

Title: US-09-524-531C-13

Perfect score: 310

Sequence: 1 MALSRRLRLRLRLPHFL.....VNYTRTSEEGDFRRKSSFVI 310

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Database size: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description            |
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| 1          | 8     | 2.6         | 146    | 2 F70313 | hypothetical prote     |
| 2          | 8     | 2.6         | 204    | 2 A88919 | conserved hypothet     |
| 3          | 8     | 2.6         | 208    | 2 D83431 | type III export pr     |
| 4          | 8     | 2.6         | 506    | 2 T02400 | probable beta-gluc     |
| 5          | 8     | 2.6         | 959    | 2 E85276 | hypothetical prote     |
| 6          | 7     | 2.3         | 118    | 1 GLYC   | gene 1 protein - S     |
| 7          | 7     | 2.3         | 128    | 2 C83448 | succinate dehydrog     |
| 8          | 7     | 2.3         | 137    | 2 B41047 | exsb protein - Pse     |
| 9          | 7     | 2.3         | 137    | 2 E83433 | exoenzyme S synthe     |
| 10         | 7     | 2.3         | 173    | 2 B90241 | hypothetical prote     |
| 11         | 7     | 2.3         | 177    | 2 E85833 | partial probable s     |
| 12         | 7     | 2.3         | 177    | 2 B90988 | hypothetical prote     |
| 13         | 7     | 2.3         | 194    | 2 T28889 | hypothetical prote     |
| 14         | 7     | 2.3         | 208    | 2 T03627 | GTP-binding protel     |
| 15         | 7     | 2.3         | 208    | 2 T01588 | GTP-binding protel     |
| 16         | 7     | 2.3         | 214    | 2 T47268 | phosphatidylserine     |
| 17         | 7     | 2.3         | 224    | 2 D71915 | phosphogluconase, cyto |
| 18         | 7     | 2.3         | 232    | 2 S60984 | hypothetical prote     |
| 19         | 7     | 2.3         | 246    | 2 F91238 | PTS system, fructo     |
| 20         | 7     | 2.3         | 246    | 2 B66086 | PTS system, fructo     |
| 21         | 7     | 2.3         | 249    | 2 G84224 | hypothetical prote     |
| 22         | 7     | 2.3         | 255    | 2 B72474 | hypothetical prote     |
| 23         | 7     | 2.3         | 267    | 2 B83705 | phosphonates trans     |
| 24         | 7     | 2.3         | 269    | 1 C69651 | prolipo-protein dia    |
| 25         | 7     | 2.3         | 280    | 2 H83623 | probable chemotaxi     |
| 26         | 7     | 2.3         | 287    | 2 E75159 | hypothetical prote     |
| 27         | 7     | 2.3         | 322    | 2 E69009 | cation antiporter      |
| 28         | 7     | 2.3         | 324    | 2 T27302 | hypothetical prote     |
| 29         | 7     | 2.3         | 332    | 1 DEBYG1 | glyceraldhyde-3-p      |

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|----|---|-----|------|----------|---------------------|
| 30 | 7 | 2.3 | 332  | 1 DEBYG2 | glyceraldhyde-3-p   |
| 31 | 7 | 2.3 | 332  | 2 C72485 | probable high-affi  |
| 32 | 7 | 2.3 | 335  | 2 S29813 | glyceraldhyde-3-p   |
| 33 | 7 | 2.3 | 337  | 2 A12360 | hypothetical prote  |
| 34 | 7 | 2.3 | 348  | 2 E84143 | L-iditol 2-dehydro  |
| 35 | 7 | 2.3 | 359  | 2 H65201 | PTS system, fructo  |
| 36 | 7 | 2.3 | 380  | 2 H75159 | 3-isopropylmalate   |
| 37 | 7 | 2.3 | 387  | 2 E90533 | nitrogen fixation   |
| 38 | 7 | 2.3 | 402  | 2 G83367 | hypothetical prote  |
| 39 | 7 | 2.3 | 421  | 2 H86217 | protein T2767.16 (  |
| 40 | 7 | 2.3 | 422  | 2 D70110 | aminotransferase (  |
| 41 | 7 | 2.3 | 429  | 2 C97500 | hypothetical prote  |
| 42 | 7 | 2.3 | 429  | 2 AC2718 | MFS permease (limo  |
| 43 | 7 | 2.3 | 445  | 2 S75859 | hypothetical prote  |
| 44 | 7 | 2.3 | 452  | 2 A70389 | seryl-tRNA(Sec) se  |
| 45 | 7 | 2.3 | 473  | 2 T28118 | hypothetical prote  |
| 46 | 7 | 2.3 | 491  | 1 O4R8PC | cytochrome P450 2B  |
| 47 | 7 | 2.3 | 491  | 2 S31277 | cytochrome P450 2B  |
| 48 | 7 | 2.3 | 491  | 2 S31278 | cytochrome P450 2B  |
| 49 | 7 | 2.3 | 491  | 2 S35666 | cytochrome P450 2B  |
| 50 | 7 | 2.3 | 505  | 2 C69666 | NADH dehydrogenase  |
| 51 | 7 | 2.3 | 512  | 2 B69146 | glutathione-regula  |
| 52 | 7 | 2.3 | 544  | 2 AE3375 | methionyl-tRNA syn  |
| 53 | 7 | 2.3 | 554  | 2 S50309 | hypothetical prote  |
| 54 | 7 | 2.3 | 573  | 2 AF1418 | ABC transporter, A  |
| 55 | 7 | 2.3 | 573  | 2 AH1793 | ABC transporter, A  |
| 56 | 7 | 2.3 | 578  | 2 G82950 | conserved hypothet  |
| 57 | 7 | 2.3 | 586  | 2 S63386 | HOL1 protein - yea  |
| 58 | 7 | 2.3 | 667  | 2 T35491 | probable serine/th  |
| 59 | 7 | 2.3 | 697  | 2 S09254 | collicin D - Escher |
| 60 | 7 | 2.3 | 703  | 2 T32572 | hypothetical prote  |
| 61 | 7 | 2.3 | 758  | 1 S45477 | SEC18 protein - ye  |
| 62 | 7 | 2.3 | 774  | 1 VPXRMT | outer layer protei  |
| 63 | 7 | 2.3 | 775  | 1 VPXRMT | outer layer protei  |
| 64 | 7 | 2.3 | 776  | 1 VPXRMT | outer layer protei  |
| 65 | 7 | 2.3 | 782  | 2 E90427 | hypothetical prote  |
| 66 | 7 | 2.3 | 805  | 2 A64453 | H+-transporting AT  |
| 67 | 7 | 2.3 | 810  | 2 AP2425 | phenylalanyl-tRNA   |
| 68 | 7 | 2.3 | 832  | 2 G97146 | probable permease   |
| 69 | 7 | 2.3 | 841  | 2 A27832 | cell division cont  |
| 70 | 7 | 2.3 | 840  | 2 T01011 | hypothetical prote  |
| 71 | 7 | 2.3 | 1105 | 2 B64973 | yeast protein - Esc |
| 72 | 7 | 2.3 | 1213 | 2 S42368 | guanine nucleotide  |
| 73 | 7 | 2.3 | 1400 | 2 A71514 | probable protein e  |
| 74 | 7 | 2.3 | 1785 | 2 T21558 | hypothetical prote  |
| 75 | 7 | 2.3 | 1929 | 2 T21559 | hypothetical prote  |

#### ALIGNMENTS

RESULT 1  
F70313  
hypothetical protein aq\_142 - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 04-Mar-2000  
C:Accession: F70313  
V:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: AF0300; MUID:98196666  
A:Accession: F70313  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-146 <AOQ>  
A:Cross-references: GB:AE000675; MID:g2982863; PIDN:AAC06501.1; PID:g2982881; GB:AE00  
A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: aq\_142  
C:Superfamily: Aquifex aeolicus hypothetical protein aq\_142

Query Match 2.68; Score 8; DB 2; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 252 LVIVLAVI 259  
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 Db 5 LVIVLAVI 12

RESULT 2  
 A89919

conserved hypothetical protein SA1250 [imported] - Staphylococcus aureus (strain N315)  
 C:Species: Staphylococcus aureus  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 C:Accession: A89919  
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
 ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Length 357; 1225-1240, 2001  
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
 A:Reference number: A89758; MUID:21311952; PMID:11418146  
 A:Accession: A89919  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-204 <KOR>  
 A:Cross-references: GB:BA000018; PID:g13701215; PIDN:BABA2510.1; GSPDB:GN00149  
 A:Experimental source: strain N315  
 C:Genetics:

A:Gene: SA1250

Query Match 2.68; Score 8; DB 2; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 3.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 IAGTIGCV 249  
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 Db 181 IAGTIGCV 188

RESULT 3  
 DB3431

type III export protein PscK PA1724 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C:Species: Pseudomonas aeruginosa  
 C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: DB3431  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
 an, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
 boy, S.; Olson, M.V.  
 Length 406; 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337  
 A:Accession: DB3431  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-208 <STO>  
 A:Cross-references: GB:AE004598; GB:AE004091; NID:99947687; PIDN:AA605113.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:

A:Gene: pscK; PA1724

Query Match 2.68; Score 8; DB 2; Length 208;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SRRRLRL 11  
 |||||  
 Db 160 SRRRLRL 167

RESULT 4  
 T02409

probable beta-glucosidase [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001  
 C:Accession: T02400; F84878  
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K  
 submitted to the EMBL Data Library, May 1998  
 A:Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.  
 A:Reference number: Z14667  
 A:Accession: T02400  
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-506 <KOR>  
 A:Cross-references: EMBL:AC004521; NID:g3128166; PIDN:AACT6091.1; PID:g3128187  
 A:Experimental source: Cultivar Columbia  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
 eus, D.; Newman, W.C.; White, O.; Eichen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
 Nature 402; 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487  
 A:Accession: F84878  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-506 <SPO>  
 A:Cross-references: GB:AE002093; NID:g3128187; PIDN:AACT6091.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: F411.26; AT2g44450  
 A:Map position: 2  
 A:Introns: 50/73; 74/1; 93/3; 119/1; 145/1; 174/2; 259/3; 370/1; 380/3; 415/1; 447/2  
 C:Superfamily: Agrobacterium beta-glucosidase

Query Match 2.68; Score 8; DB 2; Length 506;  
 Best Local Similarity 100.0%; Pred. No. 7.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 LVVIVLVA 257  
 |||||  
 Db 9 LVVIVLVA 16

RESULT 5  
 E85276

hypothetical protein AT4g24020 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 02-Mar-2001  
 C:Accession: E85276  
 R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold sp  
 Nature 402; 769-777, 1999  
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488  
 A:Accession: E85276  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-959 <SNO>  
 A:Cross-references: GB:NC\_001268; NID:g7269251; PIDN:CA8B1320.1; GSPDB:GN00140  
 C:Genetics:  
 A:Gene: AT4g24020  
 A:Map position: 4  
 C:Superfamily: Arabidopsis thaliana hypothetical protein F23E12.170

Query Match 2.68; Score 8; DB 2; Length 959;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 EAVVKKSS 37  
 |||||  
 Db 300 EAVVKKSS 307

RESULT 6  
 G1YC

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:39:47 : Search time 17.64 Seconds  
(without alignments)  
680.446 Million cell updates/sec

Title: US-09-524-531C-13

Perfect score: 310

Sequence: 1 MALSRRLRLRLRLRLPHFL.....VNYIRPSEGGDFRRKSSFV 310

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 8     | 2.6         | 146    | 1     | Y142_AQUAE  |
| 2          | 7     | 2.3         | 118    | 1     | ATP2_SYN6   |
| 3          | 7     | 2.3         | 137    | 1     | EXSB_PSEAE  |
| 4          | 7     | 2.3         | 224    | 1     | XLRI_MOUSE  |
| 5          | 7     | 2.3         | 232    | 1     | YOZ1_YEAST  |
| 6          | 7     | 2.3         | 269    | 1     | LGT_BACSU   |
| 7          | 7     | 2.3         | 280    | 1     | CHR2_PSEAE  |
| 8          | 7     | 2.3         | 331    | 1     | G3P2_YEAST  |
| 9          | 7     | 2.3         | 331    | 1     | G3P3_YEAST  |
| 10         | 7     | 2.3         | 335    | 1     | G3P1_TRIKO  |
| 11         | 7     | 2.3         | 359    | 1     | PTWC_ECOLI  |
| 12         | 7     | 2.3         | 374    | 1     | RL4_TRYBB   |
| 13         | 7     | 2.3         | 422    | 1     | CSD_BORBU   |
| 14         | 7     | 2.3         | 452    | 1     | SELA_AQUAE  |
| 15         | 7     | 2.3         | 473    | 1     | VS81_CAEEL  |
| 16         | 7     | 2.3         | 491    | 1     | CPB4_RABIT  |
| 17         | 7     | 2.3         | 491    | 1     | CPB5_RABIT  |
| 18         | 7     | 2.3         | 501    | 1     | CGAH_DROME  |
| 19         | 7     | 2.3         | 502    | 1     | CGAN_DROME  |
| 20         | 7     | 2.3         | 505    | 1     | NDHF_BACSU  |
| 21         | 7     | 2.3         | 586    | 1     | HOL1_YEAST  |
| 22         | 7     | 2.3         | 697    | 1     | CEAD_ECOLI  |
| 23         | 7     | 2.3         | 758    | 1     | SC18_YEAST  |
| 24         | 7     | 2.3         | 774    | 1     | VP4_ROTHT   |
| 25         | 7     | 2.3         | 775    | 1     | VP4_ROTHT   |
| 26         | 7     | 2.3         | 776    | 1     | VP4_ROTHT   |
| 27         | 7     | 2.3         | 840    | 1     | CC16_YEAST  |
| 28         | 7     | 2.3         | 1015   | 1     | VA17_HUMAN  |
| 29         | 7     | 2.3         | 1105   | 1     | YEGE_ECOLI  |
| 30         | 7     | 2.3         | 1234   | 1     | YMX5_CAEEL  |
| 31         | 7     | 2.3         | 2871   | 1     | FBN1_BOVIN  |
| 32         | 7     | 2.3         | 2871   | 1     | FBN1_HUMAN  |
| 33         | 7     | 2.3         | 2871   | 1     | FBN1_MOUSE  |

|    |   |     |      |   |             |
|----|---|-----|------|---|-------------|
| 34 | 7 | 2.3 | 2871 | 1 | FBN1_PIG    |
| 35 | 6 | 1.9 | 39   | 1 | PSB2_ODOSI  |
| 36 | 6 | 1.9 | 56   | 1 | SCP2_MESMA  |
| 37 | 6 | 1.9 | 56   | 1 | SCP3_MESMA  |
| 38 | 6 | 1.9 | 64   | 1 | YDT6_SCHPO  |
| 39 | 6 | 1.9 | 74   | 1 | SRP_SOYAN   |
| 40 | 6 | 1.9 | 86   | 1 | PHNP_STRNU  |
| 41 | 6 | 1.9 | 87   | 1 | PHNP_BACID  |
| 42 | 6 | 1.9 | 87   | 1 | PHNP_STRBO  |
| 43 | 6 | 1.9 | 87   | 1 | PHNP_STRSL  |
| 44 | 6 | 1.9 | 87   | 1 | Y14B_BPT4   |
| 45 | 6 | 1.9 | 89   | 1 | IAPP_FELCA  |
| 46 | 6 | 1.9 | 94   | 1 | YE23_HAEIN  |
| 47 | 6 | 1.9 | 102  | 1 | KCRB_PIG    |
| 48 | 6 | 1.9 | 105  | 1 | SP12_CAEEL  |
| 49 | 6 | 1.9 | 113  | 1 | RLJ1_SCHRO  |
| 50 | 6 | 1.9 | 118  | 1 | YKD7_YEAST  |
| 51 | 6 | 1.9 | 120  | 1 | GALP_PIG    |
| 52 | 6 | 1.9 | 126  | 1 | PFDB_SULSO  |
| 53 | 6 | 1.9 | 126  | 1 | SECE_VIBAL  |
| 54 | 6 | 1.9 | 126  | 1 | SECE_VIBCH  |
| 55 | 6 | 1.9 | 127  | 1 | Y080_MERTJ  |
| 56 | 6 | 1.9 | 130  | 1 | KV5G_MOUSE  |
| 57 | 6 | 1.9 | 130  | 1 | Y060_BPT4   |
| 58 | 6 | 1.9 | 130  | 1 | YEFQ_ECOLI  |
| 59 | 6 | 1.9 | 132  | 1 | AMP1_ALICE  |
| 60 | 6 | 1.9 | 134  | 1 | YFID_BACSU  |
| 61 | 6 | 1.9 | 137  | 1 | Y541_ARCVU  |
| 62 | 6 | 1.9 | 138  | 1 | NIKR_ARCVU  |
| 63 | 6 | 1.9 | 143  | 1 | CU17_BOMMO  |
| 64 | 6 | 1.9 | 146  | 1 | RL13_MYCCE  |
| 65 | 6 | 1.9 | 148  | 1 | PFID2_ARATH |
| 66 | 6 | 1.9 | 152  | 1 | NIKD_PSEET  |
| 67 | 6 | 1.9 | 155  | 1 | Y060_BORBU  |
| 68 | 6 | 1.9 | 157  | 1 | MEHG_MYCLE  |
| 69 | 6 | 1.9 | 160  | 1 | PETD_CHIEU  |
| 70 | 6 | 1.9 | 160  | 1 | PETD_GUTHU  |
| 71 | 6 | 1.9 | 160  | 1 | TATB_HELPJ  |
| 72 | 6 | 1.9 | 161  | 1 | ISPF_BUCAL  |
| 73 | 6 | 1.9 | 164  | 1 | RL21_ARATH  |
| 74 | 6 | 1.9 | 167  | 1 | ILVH_MYCAV  |
| 75 | 6 | 1.9 | 167  | 1 | OB_CANFA    |

#### ALIGNMENTS

|          |  |           |              |
|----------|--|-----------|--------------|
| RESULT 1 | Y142_AQUAE   | STANDARD: | PRT: 146 AA. |
| ID       | Y142_AQUAE   |           |              |
| AC       | 066537:  |           |              |
| DT       | 16-OCT-2001 (Rel. 40, Created)                                       |           |              |
| DT       | 16-OCT-2001 (Rel. 40, Last sequence update)                          |           |              |
| DE       | Hypothetical protein AO_142.   |           |              |
| OS       | Aquifex aeolicus.  |           |              |
| OC       | Bacteria; Aquificales; Aquificaceae; Aquifex.                        |           |              |
| OX       | NCBI_TaxID=63363;  |           |              |
| RP       | SEQUENCE FROM N.A.   |           |              |
| RC       | STRAIN=VF5;  |           |              |
| RA       | MEHLIN-98196666; PubMed-9337320;                                     |           |              |
| RA       | Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,      |           |              |
| RA       | Graham D.E., Overbeek R., Sneed M.A., Keller M., Aubay M., Huber R., |           |              |
| RT       | Feldman R.A., Short J.M., Olsson G.J., Swanson R.V.;                 |           |              |
| RT       | "The complete genome of the hyperthermophilic bacterium Aquifex      |           |              |
| RT       | aeolicus.";  |           |              |
| RL       | Nature 397:353-358(1998).  |           |              |

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 CC -----  
 DR EMBL: AE00675; AAC06501.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 146 AA; 16321 MW; 9E98228A820C2B2 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 252 VLIYLAVI 259  
 Db 5 VLIYLAVI 12

LT 2  
 ID \_SYNP6 STANDARD; PRT; 118 AA.  
 AC P08443;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ATP synthase protein I.  
 GN ATP1.  
 OS *Synechococcus* sp. (strain PCC 6301) (Anacystis nidulans).  
 CC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.  
 OX NCBI\_TaxID=1139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87311713; PubMed=3041005;  
 RA Cozens A.L., Walker J.E.;  
 RT "The organization and sequence of the genes for ATP synthase subunits  
 RT in the cyanobacterium *Synechococcus* 6301. Support for an  
 RT endosymbiotic origin of chloroplasts.";  
 RL J. Mol. Biol. 194:359-383(1987).  
 CC - FUNCTION: A POSSIBLE FUNCTION FOR THIS PROTEIN IS TO GUIDE THE  
 CC ASSEMBLY OF THE MEMBRANE SECTOR OF THE ATPASE ENZYME COMPLEX.  
 CC - SIMILARITY: TO THE CORRESPONDING SUBUNIT IN OTHER BACTERIA.

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 CC -----

CC EMBL: X05302; CAA28922.1; -  
 DR PIR; S10825; GIYC.  
 KW Hydrogen ion transport; CF(0); Transmembrane.  
 FT TRANSMEM 11 31 POTENTIAL.  
 FT TRANSMEM 73 93 POTENTIAL.  
 FT TRANSMEM 94 114 POTENTIAL.  
 SQ SEQUENCE 118 AA; 13455 MW; 16B76A47F76CC196 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 251 VLIYLAVI 257  
 Db 75 VLIYLAVI 81

RESULT 3  
 EXSB\_PSEAE STANDARD; PRT; 137 AA.  
 ID EXSB\_PSEAE  
 AC P26994;

DT 01-AUG-1992 (Rel. 23, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Exoenzyme S synthesis protein B.  
 GN EXSB OR PA1712.  
 OS *Pseudomonas aeruginosa*.  
 CC Bacteria; Proteobacteria; gamma subdivision; *Pseudomonadaceae*;  
 CC *Pseudomonas*.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=92011420; PubMed=1655713;  
 RA Frank D.W., Iglewski B.H.;  
 RT "Cloning and sequence analysis of a trans-regulatory locus required  
 RT for exoenzyme S synthesis in *Pseudomonas aeruginosa*.";  
 RL J. Bacteriol. 173:6460-6468(1991).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stever C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.V., Coulter S.N., Folger K.R., Kas A., Lartig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 CC - SIMILARITY: TO Y. ENTEROCOLITICA VIRB.

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 CC -----

CC EMBL: M64975; AAA25815.1; -  
 DR EMBL: AE004597; AAG05101.1; -  
 DR PIR; B41047; BA1047.  
 KW Complete proteome.  
 FT CONFLICT 62 R -> W (IN REF. 1).  
 FT SEQUENCE 137 AA; 14996 MW; F7367E7AB301C4EA CRC64;

Query Match 2.3%; Score 7; DB 1; Length 137;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LRLRLVA 13  
 Db 41 LRLRLVA 47

RESULT 4  
 XLRL\_MOUSE STANDARD; PRT; 224 AA.  
 ID XLRL\_MOUSE  
 AC 092114;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE X-linked juvenile retinoschisis protein precursor.  
 GN RSL1 OR RSLH OR XLRL1.  
 OS *Mus musculus* (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ;

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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:38:12 ; Search time 48.09 Seconds

(without alignments)  
1115.168 Million cell updates/sec

Title: US-09-524-531C-13

Perfect score: 310  
Sequence: 1 MALSRRLRLVRLPHEFL.....VNYIRNSEGDFRHSSEFVI 310

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mnc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_todent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 253   | 81.6        | 310    | 11    | Q9EPK4 mus musculu |
| 2          | 245   | 79.0        | 310    | 11    | Q9D1M9 mus musculu |
| 3          | 152   | 49.0        | 310    | 11    | Q9DBB7 mus musculu |
| 4          | 24    | 7.7         | 309    | 4     | Q96FL1 homo sapien |
| 5          | 24    | 7.7         | 310    | 4     | Q9BX67             |
| 6          | 8     | 2.6         | 204    | 16    | Q99U70 homo sapien |
| 7          | 8     | 2.6         | 206    | 2     | P95439 staphylococ |
| 8          | 8     | 2.6         | 208    | 16    | Q91313 pseudomonas |
| 9          | 8     | 2.6         | 246    | 5     | Q9XV46 ctenocephal |
| 10         | 8     | 2.6         | 400    | 10    | Q91T44 arabidopsi  |
| 11         | 8     | 2.6         | 506    | 10    | Q64879 arabidopsi  |
| 12         | 8     | 2.6         | 959    | 10    | Q22987 arabidopsi  |
| 13         | 7     | 2.3         | 85     | 12    | Q99CX8 heliocoverp |
| 14         | 7     | 2.3         | 95     | 10    | Q9FE08 perilla fru |
| 15         | 7     | 2.3         | 121    | 2     | Q93H04 streptococ  |
| 16         | 7     | 2.3         | 125    | 11    | Q9CS62 mus musculu |

#### ALIGNMENTS

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
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| 17  | 18  | 19  | 20  | 21  | 22  | 23  | 24  | 25  | 26  | 27  | 28  | 29  | 30  | 31  | 32  | 33  | 34  | 35  | 36  | 37  | 38  | 39  | 40  | 41  | 42  | 43  | 44  | 45  | 46  | 47  | 48  | 49  | 50  | 51  | 52  | 53  | 54  | 55  | 56  | 57  | 58  | 59  | 60  | 61  | 62  | 63  | 64  | 65  | 66  | 67  | 68  | 69  | 70  | 71  | 72  | 73  | 74  | 75  |     |     |     |     |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   | 7   |     |     |     |     |     |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| 128 | 147 | 173 | 177 | 194 | 208 | 208 | 214 | 220 | 224 | 224 | 232 | 242 | 247 | 249 | 255 | 255 | 267 | 269 | 273 | 274 | 280 | 280 | 281 | 281 | 284 | 287 | 291 | 314 | 322 | 324 | 324 | 332 | 337 | 339 | 345 | 348 | 354 | 354 | 375 | 375 | 376 | 376 | 380 | 387 | 402 | 405 | 405 | 411 | 421 | 430 | 445 | 484 | 491 | 497 | 500 | 512 | 530 | 532 |     |     |     |     |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11036763;
RA Aitrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAW-2 and JAW-3: an Emerging Junctional Adhesion Molecular
  Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RX EMBL: AJ300304; CAC20704.1;
DR MGD; MGI:1933820; Jcma2.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_c2.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00409; Ig_2.
DR SMART: SM00408; IgC2; 2.
DR SMART: SM00410; Ig_1like; 1.
KW Immunoglobulin domain.
SQ
SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;
Query Match 81.6%; Score 253; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.5e-252;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE 1110002N23RIK PROTEIN.
GN JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
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RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RX EMBL: AK003326; BAB22715.1;
DR MGD; MGI:1933820; Jcma2.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_c2.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00409; Ig_2.
DR SMART: SM00408; IgC2; 2.
DR SMART: SM00410; Ig_1like; 1.
KW Immunoglobulin domain.
SQ
SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;
Query Match 79.0%; Score 245; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.8e-244;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 298 EECDF 302

RESULT 3  
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 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE 1110002N23RIK PROTEIN.  
 GN JCAM2 OR 1110002N23RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxId=10090;  
 RN [1]

SEQUENCE FROM N.A.  
 STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;  
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 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,  
 Kuehl P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,  
 Schirml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,  
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasaki H., Sato K., Schenbach C., Sessa T., Shibata Y., Storch K.-F.,  
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection."  
 RA Nature 409:685-690(2001).  
 RL EMBL: AK008187; BAB2519.1; -;  
 DR MGD: MGI:1933820; Jcam2.  
 DR InterPro: IPR003598; I9.  
 DR InterPro: IPR003598; I9.  
 DR InterPro: IPR003600; I9.C2.  
 DR InterPro: IPR003600; I9.Like.  
 DR InterPro: IPR003006; I9\_MHC.  
 PLam: PF00047; I9; 2.  
 SMART: SM00409; I9; 2.  
 SMART: SM00408; IGC2; 2.  
 SMART: SM00410; IG.Like; 1.  
 DR Immunoglobulin domain.  
 KW  
 SQ SEQUENCE 310 AA: 34855 MW: C74884EABE234680 CRC64;

Query Match 49.0%; Score 152; DB 11; Length 310;  
 Best Local Similarity 99.6%; Pred. No. 2.6e-148;  
 Matches 252; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 58 SOTSDBRIEMKKIQQDQTYVYFDNKTQDLAGRTDVGKTSIRINWTRSDSAIRCEV 117  
 Db 58 SOTSDBRIEMKKIQQDQTYVYFDNKTQDLAGRTDVGKTSIRINWTRSDSAIRCEV 117  
 OY 118 VALNDKREYDEITIELIVYKPYTPVCRIPAAVPGKATLQCESEGYPRPHYSYRND 177  
 Db 118 VALNDKREYDEITIELIVYKPYTPVCRIPAAVPGKATLQCESEGYPRPHYSYRND 177  
 OY 178 VPLPTDSRANPRFONSSFFVNSSETGLVFNNAVHKKDSGGYTCASNDADAAREGDDMEV 237  
 Db 178 VPLPTDSRANPRFONSSFFVNSSETGLVFNNAVHKKDSGGYTCASNDADAAREGDDMEV 237  
 OY 238 YDLNAGIIGGVLLVLAIVITMGICAYRRGCFISSKODESEYKSPCKHGDVNYIRTS 297

Db 238 YDLNAGIIGGVLLVLAIVITMGICAYRRGCFISSKODESEYKSPCKHGDVNYIRTS 297  
 OY 298 EECDFRRKSSFYI 310  
 Db 298 EECDFRRKSSFYI 310

RESULT 4  
 ID 096FL1 PRELIMINARY: PRT: 309 AA.  
 AC 096FL1:  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE UNKNOWN (PROTEIN FOR IMAGE:3875338) (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=EYE, AND RETINOBLASTOMA.  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC010690; AAH10690.1; -;  
 FT NON\_TER 1 1  
 SQ SEQUENCE 309 AA: 34917 MW: 50C5B1B78728BDF3 CRC64;

Query Match 7.7%; Score 24; DB 4; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 PRPHYSYRNDVPLPTDSRANPRF 190  
 Db 166 PRPHYSYRNDVPLPTDSRANPRF 189

RESULT 5  
 ID 09BX67 PRELIMINARY: PRT: 310 AA.  
 AC 09BX67:  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE JUNCTIONAL ADHESION MOLECULE 3 PRECURSOR (JUNCTIONAL ADHESION MOLECULE-2).  
 GN JAM-2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRIN;  
 RA Cunningham S.A., Arrate M.P., Tran T.M.;  
 RL "Cloning of Human Junctional Adhesion Molecule 3."  
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Aurand-Lions M.A., Johnson-Leger C., Wong C., Dupasquier L.;  
 RT "Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM family members."  
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Aurand-Lions M.A., Johnson-Leger C., Lamagna C., Ozaki H., Kita T.;  
 RT "Junctional adhesion molecules (JAMs) and Interendothelial junctions."  
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF356518; AAK27221.1; -;

DR EMBL: AJ344431; CAC69845.1; -  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00408; IgC2; 2.  
 DR SMART: SM00410; Ig\_Like; 1.  
 KM Immunoglobulin domain; Signal.  
 FT SIGNAL 1 30  
 SQ SEQUENCE 310 AA; 35020 MW; CE39ADF3EALDAB9 CRC64;

Query Match 7.7%; Score 24; DB 4; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190  
 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 6  
 ID Q99U70 PRELIMINARY; PRT; 204 AA.  
 AC Q99U70;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CONSERVED HYPOTHETICAL PROTEIN (HYPOTHETICAL PROTEIN SAV1417).  
 GN SA1250 OR SAV1417.  
 OS Staphylococcus aureus (strain N315), and  
 OC Staphylococcus aureus (strain Mu50).  
 CC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 CC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=158879, 158878;  
 RX MEDLINE=21311952; PubMed=11418146;  
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,  
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,  
 RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,  
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,  
 RA Hattori M., Ogasawara N., Hayashi H., Hirata S. K.;  
 "Whole genome sequencing of methicillin-resistant Staphylococcus  
 aureus."  
 RL Lancet 357:1225-1240(2001).  
 DR EMBL: AP003133; BAB42510.1;  
 DR EMBL: AP003362; BAB57579.1;  
 DR InterPro: IPR000326; PA\_PTPase.  
 DR Pfam: PF01569; PAP2; 1.  
 DR SMART: SM00014; acidppc; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 204 AA; 22685 MW; 009CF65DB1PBDP2 CRC64;

Query Match 2.6%; Score 8; DB 16; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IAGTIGGV 249  
 181 IAGTIGGV 188

RESULT 7  
 ID P95439 PRELIMINARY; PRT; 206 AA.  
 AC P95439;

DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE PSCK.  
 GN PSCK.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 CC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=388;  
 RX MEDLINE=97126825; PubMed=8971719;  
 RA Yahr T.L., Goranson J., Frank D.W.;  
 RT "Exoenzyme S of Pseudomonas aeruginosa is secreted by a type III  
 RT pathway".  
 RL Mol. Microbiol. 22:991-1003(1996).  
 DR EMBL: U56077; AAC44782.1;  
 SQ SEQUENCE 206 AA; 23971 MW; 8DDDE751E26BDFR8 CRC64;

Query Match 2.6%; Score 8; DB 2; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 7.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRRRLRL 11  
 160 SRRRLRL 167

RESULT 8  
 ID Q91313 PRELIMINARY; PRT; 208 AA.  
 AC Q91313;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE TYPE III EXPORT PROTEIN PSCK.  
 GN PSCK OR PA1724.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 CC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Slover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody K.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen."  
 RL Nature 406:959-964(2000).  
 DR EMBL: AE004598; AAC05113.1;  
 KW Complete proteome.  
 SQ SEQUENCE 208 AA; 23898 MW; 74F6B5848FE9E5BE CRC64;

Query Match 2.6%; Score 8; DB 16; Length 208;  
 Best Local Similarity 100.0%; Pred. No. 7.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRRRLRL 11  
 160 SRRRLRL 167

RESULT 9  
 ID Q9XY46 PRELIMINARY; PRT; 246 AA.  
 AC Q9XY46;